

# SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

## STAFF USE ONLY

Date completed: 07-07-04  
Searcher: Beverly C 2528  
Terminal time: 20  
Elapsed time: \_\_\_\_\_  
CPU time: \_\_\_\_\_  
Total time: 25  
Number of Searches: \_\_\_\_\_  
Number of Databases: 1

### Search Site

\_\_\_\_\_ STIC  
\_\_\_\_\_ CM-1  
\_\_\_\_\_ Pre-S

### Type of Search

\_\_\_\_\_ N.A. Sequence  
\_\_\_\_\_ A.A. Sequence  
\_\_\_\_\_ Structure  
\_\_\_\_\_ Bibliographic

### Vendors

\_\_\_\_\_ IG  
\_\_\_\_\_ STN  
\_\_\_\_\_ Dialog  
\_\_\_\_\_ APS  
\_\_\_\_\_ Geninfo  
\_\_\_\_\_ SDC  
\_\_\_\_\_ DARC/Questel  
☒ Other CGN

STIC-Biotech/ChemLib

126063

From: Ramirez, Delia  
Sent: Wednesday, June 30, 2004 11:45 AM  
To: STIC-Biotech/ChemLib  
Subject: case 09/762,258

Hi,

I would like to request the following interference search:

1. seq id 1 and 2 in the nucleic acid databases
2. seq id 2 in the protein databases

Thank you,

Delia M. Ramirez, Ph.D.  
Patent Examiner  
Recombinant Enzymes-Art Unit 1652  
USPTO  
400 Dulany Street, Remsen Bldg., 3A74, Mail room 3C70  
Alexandria, VA 22314  
(571) 272-0938  
delia.ramirez@uspto.gov

RECEIVED  
JUN 30 2004  
STIC

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 16:54:07 ; Search time 23 Seconds  
(without alignments)

1111.081 Million cell updates/sec

Title: US-09-762-258-2

2614

Perfect score: 1 MARGRRARAGAAVAAPFDL.....PIRPSGTGKSKRGKRGKGR 495

Sequence:

BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 369414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 369414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2614	100.0	495	4	US-09-430-564-3
2	2551	97.6	482	4	US-09-430-564-2
3	1749	66.9	525	2	US-08-749-902-8
4	1747	66.8	525	2	US-08-749-902-7
5	1747	66.8	525	4	US-09-430-564-16
6	1428	54.6	637	4	US-09-817-310-2
7	1415	54.1	268	4	US-09-430-564-12
8	1385.5	53.0	495	2	US-08-749-902-3
9	1354	51.8	258	4	US-09-430-564-6
10	806.5	30.9	431	4	US-09-031-295-2
11	802.5	30.7	431	2	US-08-712-709-5
12	802.5	30.7	431	2	US-09-111-444-5
13	802.5	30.7	431	2	US-09-541-228-5
14	791	30.3	430	2	US-08-712-709-5
15	791	30.3	430	3	US-09-111-444-9
16	791	30.3	430	3	US-09-541-228-9
17	763	29.2	726	4	US-09-417-197-71
18	762	29.2	480	3	US-09-091-058-2
19	762	29.2	727	4	US-09-417-197-139
20	701.5	26.8	587	1	US-08-313-274-2
21	699.5	26.8	671	6	5266464-2
22	697	26.7	942	4	US-08-685-852-3
23	696	26.6	916	4	US-09-417-197-73
24	683	26.1	737	4	US-09-772-647-4
25	678	25.9	1151	4	US-09-457-0408-11
26	650	24.9	584	4	US-09-842-307-2
27	622.5	23.8	343	4	US-09-394-455-15

#### ALIGNMENTS

28	618.5	23.7	350	4	US-09-457-0408-37	Sequence 37, Appli
29	618.5	23.7	351	4	US-09-457-0408-6	Sequence 6, Appli
30	617.5	23.6	336	4	US-09-394-455-2	Sequence 2, Appli
31	617.5	23.6	343	4	US-09-394-455-34	Sequence 34, Appli
32	617.5	23.6	343	4	US-09-394-455-38	Sequence 38, Appli
33	617.5	23.6	351	4	US-09-394-455-38	Sequence 4, Appli
34	617.5	23.6	359	4	US-09-417-197-69	Sequence 69, Appli
35	616.5	23.6	932	4	US-09-417-197-137	Sequence 137, App
36	616.5	23.6	931	4	US-09-417-197-135	Sequence 135, App
37	615	23.5	676	3	US-09-313-930-2	Sequence 7, Appli
38	610.5	23.4	260	2	US-07-857-2248-7	Sequence 8, Appli
39	602.5	23.0	260	2	US-07-857-2248-8	Sequence 6, Appli
40	601.5	23.0	260	2	US-07-857-2248-6	Sequence 15, Appli
41	588.5	22.5	264	2	US-07-857-2248-15	Sequence 10, Appli
42	587.5	22.5	264	2	US-07-857-2248-10	Sequence 14, Appli
43	581	22.2	269	2	US-07-857-2248-14	Sequence 1, Appli
44	578.5	22.1	260	2	US-07-857-2248-1	Sequence 13, Appli
45	577.5	22.1	263	2	US-07-857-2248-13	

  

RESULT 1	US-09-430-564-3
Sequence 3, Application US/09430564	
Patent No. 6372467	
GENERAL INFORMATION:	
APPLICANT: John Blenis	
APPLICANT: Kay K. Lee-Fruman	
APPLICANT: Calvia J. Kuo	
TITLE OR INVENTION: P5456K AND P856K GENES, PROTEINS,	
FILE REFERENCE: 00246/506002	
CURRENT APPLICATION NUMBER: US/09/430,564	
PRIOR FILING DATE: 1999-10-29	
NUMBER OF SEQ ID NOS: 16	
SOFTWARE: FASTSEQ for Windows Version 4.0	
SEQ ID NO 3	
LENGTH: 495	
TYPE: PRT	
ORGANISM: Homo sapiens	
US-09-430-564-3	

  

Query Match	100.0%	Score 2614	DB 4	Length 495
Best Local Similarity	100.0%	Pred. No. 4.3e-209	Indels 0	Gaps 0
Matches 495	Conservative 0	Mismatches 0		

  

QY	1	MARGRRARAGAAVAAPFDLDEETBEGSEGEPELSPADACPLAELRAAGLSPVGHYEE	60
DB	1	MARGRRARAGAAVAAPFDLDEETBEGSEGEPELSPADACPLAELRAAGLSPVGHYEE	60
QY	61	VELTETSVNVPERRIPGHCBELRLVIGKGYGVKRVKVOGTNLKITYAMKVLRAKIV	120
DB	61	VELTETSVNVPERRIPGHCBELRLVIGKGYGVKRVKVOGTNLKITYAMKVLRAKIV	120
QY	61	VELTETSVNVPERRIPGHCBELRLVIGKGYGVKRVKVOGTNLKITYAMKVLRAKIV	120
DB	61	VELTETSVNVPERRIPGHCBELRLVIGKGYGVKRVKVOGTNLKITYAMKVLRAKIV	120
QY	121	RNAKQFAHRABNITLESVHPPIVELAFAFOTGKLYILICLSGGEFTLHERGIFL	180
DB	121	RNAKQFAHRABNITLESVHPPIVELAFAFOTGKLYILICLSGGEFTLHERGIFL	180
QY	121	RNAKQFAHRABNITLESVHPPIVELAFAFOTGKLYILICLSGGEFTLHERGIFL	180
DB	121	RNAKQFAHRABNITLESVHPPIVELAFAFOTGKLYILICLSGGEFTLHERGIFL	180
QY	181	EDTACFYALBITLALGHSOGIYYDLNPNIMLSSQGHKLTDFGLCKESIHEGAVTH	240
DB	181	EDTACFYALBITLALGHSOGIYYDLNPNIMLSSQGHKLTDFGLCKESIHEGAVTH	240
QY	181	EDTACFYALBITLALGHSOGIYYDLNPNIMLSSQGHKLTDFGLCKESIHEGAVTH	240
DB	181	EDTACFYALBITLALGHSOGIYYDLNPNIMLSSQGHKLTDFGLCKESIHEGAVTH	240
QY	241	TTCGTEWAPRELIVSGNRAVDWMSLCAIWMYDUTGSPPTAENRKKTMKIIIRGKA	300
DB	241	TTCGTEWAPRELIVSGNRAVDWMSLCAIWMYDUTGSPPTAENRKKTMKIIIRGKA	300
QY	241	TTCGTEWAPRELIVSGNRAVDWMSLCAIWMYDUTGSPPTAENRKKTMKIIIRGKA	300
DB	241	TTCGTEWAPRELIVSGNRAVDWMSLCAIWMYDUTGSPPTAENRKKTMKIIIRGKA	300
QY	301	LPPEYLPDARDLVKFLKXNPSQRIQGGPGDAADYQRFHFFRRNMWDLLAARVDPFPRP	360
DB	301	LPPEYLPDARDLVKFLKXNPSQRIQGGPGDAADYQRFHFFRRNMWDLLAARVDPFPRP	360
QY	301	LPPEYLPDARDLVKFLKXNPSQRIQGGPGDAADYQRFHFFRRNMWDLLAARVDPFPRP	360
DB	301	LPPEYLPDARDLVKFLKXNPSQRIQGGPGDAADYQRFHFFRRNMWDLLAARVDPFPRP	360

QY 361 CLOSEBVSQDPTFTQTPVDSDDTALSESANQALGFTYVAPSLDSIKGFSFQPK 420  
 DB 361 CLOSEBVSQDPTFTQTPVDSDDTALSESANQALGFTYVAPSLDSIKGFSFQPK 420  
 QY 421 LRSRRRLNSSRRVSVSLKSPFEGFRSPSLPPTLPLPPLPPPPSTTAPLPTRP 480  
 DB 421 LRSRRRLNSSRRVSVSLKSPFEGFRSPSLPPTLPLPPLPPPPSTTAPLPTRP 480  
 QY 481 SGTGKSKRGGRGPR 495  
 DB 481 SGTGKSKRGGRGPR 495

RESULT 2  
 US-09-430-564-2  
 ; Sequence 2, Application US/09340564  
 ; Patent No. 6372467  
 ; GENERAL INFORMATION:  
 ; APPLICANT: John Blenis  
 ; APPLICANT: Kay K. Lee-Fruman  
 ; APPLICANT: Calvin J. Kuo  
 ; TITLE OF INVENTION: P54S6K AND P85S6K GENES, PROTEINS,  
 ; FILE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS  
 ; FILE REFERENCE: 00246/506002  
 ; CURRENT APPLICATION NUMBER: US/09/430,564  
 ; PRIOR FILING DATE: 1999-10-29  
 ; PRIOR APPLICATION NUMBER: 60/106,141  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 482  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-430-564-2

Query Match 97.6%; Score 2551; DB 4; Length 482;  
 Best Local Similarity 100.0%; Pred. No. 7, 2e-204;  
 Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MAAPFDLDLTERGSGEGEPBLSPADACPLAELRAAGLEPVGHYEVELETSTVAVGE 73  
 DB 1 MAAPFDLDLTERGSGEGEPBLSPADACPLAELRAAGLEPVGHYEVELETSTVAVGE 60  
 QY 74 RIGPHCELLRVLGKGGYGVFQVRKVOGNTLGIYAMKYLRAKIVRAKOTATRRAR 133  
 DB 61 RIGPHCELLRVLGKGGYGVFQVRKVOGNTLGIYAMKYLRAKIVRAKOTATRRAR 120  
 QY 134 NILESVAHPPIVELAAYAFOTGALYILBCLSGELFTLBRGIFLEDTACFYLAETL 193  
 DB 121 NILESVAHPPIVELAAYAFOTGALYILBCLSGELFTLBRGIFLEDTACFYLAETL 180  
 QY 194 ALGHLSOGITVNDLPEENIMSSOGHITLTDGCLKESHEGAVHTGCTEYVAPEI 253  
 DB 181 ALGHLSOGITVNDLPEENIMSSOGHITLTDGCLKESHEGAVHTGCTEYVAPEI 240  
 QY 254 LVASGNRAVDWMSLGLMYDMLTGSPPFAENRKKXTMXIRGKALAPPIYLPDARDIV 313  
 DB 241 LVASGNRAVDWMSLGLMYDMLTGSPPFAENRKKXTMXIRGKALAPPIYLPDARDIV 300  
 QY 314 KXFLKKNPQORIGGGKADADVORHFFETAMVDLLARVDPFPRCLOSEEDVSQFDT 373  
 DB 301 KXFLKKNPQORIGGGKADADVORHFFETAMVDLLARVDPFPRCLOSEEDVSQFDT 360  
 QY 374 RFRQTPVDSDDTALSESANQALGFTYVAPSLDSIKGFSFQPKLSPRLNNSPV 433  
 DB 361 RFRQTPVDSDDTALSESANQALGFTYVAPSLDSIKGFSFQPKLSPRLNNSPV 420  
 QY 434 PVSPLKSPFEGFRSPSLPPTLPLPPLPPPPSTTAPLPTRP 493  
 DB 421 PVSPLKSPFEGFRSPSLPPTLPLPPLPPPPSTTAPLPTRP 480

QY 494 GR 495  
 DB 481 GR 482

RESULT 3  
 US-08-749-902-8  
 ; Sequence 8, Application US/08749902  
 ; Patent No. 5985635  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bandman, Olga  
 ; APPLICANT: Golt, Surya K.  
 ; APPLICANT: Hillman, Jennifer L.  
 ; TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: US  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/749,902  
 ; FILING DATE: Filed Herewith  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0150 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-855-0555  
 ; TELEFAX: 415-845-4166  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 525 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GenBank  
 ; CLONE: 1562  
 ; US-08-749-902-8

Query Match 56.9%; Score 1749; DB 2; Length 525;  
 Best Local Similarity 68.2%; Pred. No. 3, 6e-137;  
 Matches 350; Conservative 51; Mismatches 82; Indels 30; Gaps 8;

QY 1 MARGRRAGAGAA-----MAAPFDLDLTERGSGEGEPBLSPADACPLAE-LRA 49  
 DB 1 MARRRRRGGFPAPDPFRBAEDNAGVFDIDLDQEDAGSDELE-----EGGQINBSMDH 56  
 QY 50 AGLB-----VGHYEVELETSTVAVGPERIGPHCELLRVLGKGGYGVFQVRKVOGNTL 105  
 DB 57 GGVGPEYELGMEHCEKEFETSETSVNGPKIRPECELLRVLGKGGYGVFQVRKVOGNTL 116  
 QY 106 GKIYAMKYLRAKIVRAKOTATRRARNTLESVHPPIVELAAYAFOTGALYILBCL 165  
 DB 117 GKIYAMKYLRAKIVRAKOTATRRARNTLESVHPPIVELAAYAFOTGALYILBCL 176  
 QY 166 GGEFLTHLRGCIPLIEDTACFYLAETLALGHLSOGITVNDLPEENIMSSOGHITLTD 225  
 DB 177 GGEFLTHLRGCIPLIEDTACFYLAETLALGHLSOGITVNDLPEENIMSSOGHITLTD 236  
 QY 226 FGLCKESHEGAVHTGCTEYVAPEILVSGNRAVDWMSLGLMYDMLTGSPPFAE 285

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D 237 FGLCKSEIHGDTVHTTCGTLIEYMAPEILKSSGNRAVDWMSLGALHTDLPAPPTGE 236
Q 286 NRKXTMDKIRGKLALPPLYLPDARDLVKFFLKRNPSQRIQGGPGDAADVQRRPFRHNN 345
D 297 NRKXTIDKILKCKMLPPYLTQEARDLKLLKNNASRLGAGPGDAGVQAHPPFRHIN 356
Q 346 MDLLAMRVDPPEPPCLQSEEDVSGPDTREFTROTVPVSPDDTALSANQAFLGFTTVAP 405
D 357 WEELAKRVKPEPPKPLQSEEDVSGPDSKFTROTVPVSPDDTALSANQVFLGFTTVAP 416
Q 406 SVLDSIKEGSFQPKLSPRLNNSPRVPSPLKFSPE---GFRPSPLPE-PTLPL 460
D 417 SVLESVKEKFSPEPKIRSPRRFGSPRTVPSPVKFSFGDFMGASASTANPQTPVEYPM 476
Q 461 PPLPPEPSTT-----APLPIRP-SGTKSK 487
D 477 ETSGIEQMDVYTGSAAPLPIRQPNSGPYKKQ 509

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## RESULT 4

```

US-08-749-902-7
Sequence 7, Application US/08749902
Patent No. 5985635
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,902
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0150 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 525 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONING: 189508
US-08-749-902-7

```

```

Query Match 66.8%; Score 1747; DB 2; Length 525;
Best Local Similarity 67.9%; Pred. No. 5.2e-137;
Matches 351; Conservative 49; Mismatches 79; Indels 38; Gaps 8;

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Q 1 MARGRRARAGAA-----MAAVFDLLETBEGSGEGPELSPADACPLAE-LRA 49

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D 1 MRRRRRDGFYPAEDFRDRAEMAGVFDIDDQPPDASSDELE----EGGQANESKH 56
Q 50 AGLRP-----VGHYEVELTETSUNVGPERIGHCFELLAVLKGXGYGVYKVRKQGTNL 105
D 57 GGVGPEYELGMEHCHEKEKEISETSVNRGPEKIRPECFELLAVLKGXGYGVYKVRKQGTNT 116
Q 106 GKTYAKVLRKAKTVANAKDTAHTRAERNILSVKRPFLVEALAYAFQTGKLYLILEGCS 165
D 117 GKTFPAKVLKAKMTVANAADTAHTTAERNILSEVKRPFLVDLYAFQTGKLYLILEYLS 176
Q 166 GSELFTHLRREGIFLEDACFYLAETITLALGHLSGGIYRDKPENIMLSGGHILKTD 225
D 177 GSELFTHLRREGIFLEDACFYLAETITLALGHLSGGIYRDKPENIMILNQGKVLTD 236
Q 226 FGLCKSEIHGAVTHTFCCTIETMAPEILVYRGHRAVUWMSLGALMYKLTGSPPTAE 285
D 237 FGLCKSEIHGDTVHTTCGTLIEYMAPEILKRNPSQRIQGGPGDAADVQRRPFRHNN 296
Q 286 NRKXTMDKIRGKLALPPLYLPDARDLVKFFLKRNPSQRIQGGPGDAADVQRRPFRHNN 345
D 297 NRKXTIDKILKCKMLPPYLTQEARDLKLLKNNASRLGAGPGDAGVQAHPPFRHIN 356
Q 346 MDLLAMRVDPPEPPCLQSEEDVSGPDTREFTROTVPVSPDDTALSANQAFLGFTTVAP 405
D 357 WEELAKRVKPEPPKPLQSEEDVSGPDSKFTROTVPVSPDDTALSANQVFLGFTTVAP 416
Q 406 SVLDSIKEGSFQPKLSPRLNNSPRVPSPLKFSPE---FEGFRPSPLPEPTLPLPL 463
D 417 SVLESVKEKFSPEPKIRSPRRFGSPRTVPSPVKFSFGDFMGASAS----TANQTV 472
Q 464 LPPEPSS-----TAPLPIRP-SGTKSK 487
D 473 EYFMETSGIEQMDVYTGSAAPLPIRQPNSGPYKKQ 509

```

## RESULT 5

```

US-09-430-564-16
Sequence 16, Application US/09430564
Patent No. 6372467
GENERAL INFORMATION:
APPLICANT: John Blenis
APPLICANT: Kay K. Lee-Fruman
APPLICANT: Calvin J. Kuo
TITLE OF INVENTION: P54S6K AND P85S6K GENES, PROTEINS,
TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
FILE REFERENCE: 00246/506002
CURRENT APPLICATION NUMBER: US/09/430,564
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/106,141
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
US-09-430-564-16

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Query Match 66.8%; Score 1747; DB 4; Length 525;
Best Local Similarity 67.9%; Pred. No. 5.2e-137;
Matches 351; Conservative 49; Mismatches 79; Indels 38; Gaps 8;

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Q 1 MARGRRARAGAA-----MAAVFDLLETBEGSGEGPELSPADACPLAE-LRA 49
D 1 MRRRRRDGFYPAEDFRDRAEMAGVFDIDDQPPDASSDELE----EGGQANESKH 56
Q 50 AGLRP-----VGHYEVELTETSUNVGPERIGHCFELLAVLKGXGYGVYKVRKQGTNL 105
D 57 GGVGPEYELGMEHCHEKEKEISETSVNRGPEKIRPECFELLAVLKGXGYGVYKVRKQGTNT 116
Q 106 GKTYAKVLRKAKTVANAKDTAHTRAERNILSVKRPFLVEALAYAFQTGKLYLILEGCS 165
D 117 GKTFPAKVLKAKMTVANAADTAHTTAERNILSEVKRPFLVDLYAFQTGKLYLILEYLS 176

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QY 166 GGEFTLHREBGFLEBDTACPYLAITLALGHLSGGIITRDLPENITLSSGCHITLND 225  
 DB 177 GGEFTLHREBGFLEBDTACPYLAITLALGHLSGGIITRDLPENITLSSGCHITLND 236  
 QY 226 FGLCKESIHEGAVTHTECGTIEYAPPELVASGNNRAVDMWSLGAALYDMLTJGSPPTAE 285  
 DB 237 FGLCKESIHEGAVTHTECGTIEYAPPELVASGNNRAVDMWSLGAALYDMLTJGSPPTAE 296  
 QY 286 NRKXTMDKIRKXALPPLYTPDARDLVKKFLKKNPSQRIQGGPGDAADVQRHFFRHMN 345  
 DB 297 NRKXTMDKIRKXALPPLYTPDARDLVKKFLKKNPSQRIQGGPGDAADVQRHFFRHMN 356  
 QY 346 WDDLAWRVPPRPPCLOSEEDVSQDFEFTROTVPVSDTLSSANQAFGPTVAP 405  
 DB 357 WDDLAWRVPPRPPCLOSEEDVSQDFEFTROTVPVSDTLSSANQAFGPTVAP 416  
 QY 406 SVLDSINEGFSFOKLSPRRLNSSPRVPSPLKSP--FEGFRPSPLEPTELPPL 463  
 DB 417 SVLDSINEGFSFOKLSPRRLNSSPRVPSPLKSP--FEGFRPSPLEPTELPPL 472  
 QY 464 LPPPPS-----TTAPPIPP--SGTKSK 487  
 DB 473 EYMETSGIEQMDVMSGASAPLPIRQNSGPKKQ 509

## RESULT 6

US-09-817-310-2  
 ; Sequence 2, Application US/09817310  
 ; Patent No. 6534311  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stewart, Mary  
 ; APPLICANT: Kozma, Sarah  
 ; APPLICANT: Thomas, George  
 ; TITLE OF INVENTION: Drosophila melanogaster P70 S6 Kinase  
 ; FILE REFERENCE: 4-20371/A  
 ; CURRENT APPLICATION NUMBER: US/09/817,310  
 ; CURRENT FILING DATE: 2001-03-26  
 ; PRIOR APPLICATION NUMBER: 09/230,247  
 ; PRIOR FILING DATE: 1999-04-16  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: Patentn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 637  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 US-09-817-310-2

Query Match 54.6%; Score 1428; DB 4; Length 637;  
 Best Local Similarity 67.2%; Pred. No. 2.2e-110;  
 Matches 279; Conservative 47; Mismatches 81; Indels 8; Gaps 4;

QY 19 DLELETEEGSEGEGB-ELSPADACPLAEPLRAAGLEPVGHYEVELETETSVNVPRIQP 77  
 DB 17 DLELETEEGSEGEGB-ELSPADACPLAEPLRAAGLEPVGHYEVELETETSVNVPRIQP 74  
 QY 78 HCEFLRLVTLGKGYGVQVRKVQGTNGLKIYAMKVLRAKIYRANADTAHTRAEINLIE 137  
 DB 75 HCEFLRLVTLGKGYGVQVRKVQGTNGLKIYAMKVLRAKIYRANADTAHTRAEINLIE 134  
 QY 138 SVHGPPIVELAVALFOTGKLYLLECLSGGELFTLHREBGFLEBDTACPYLAITLALGH 197  
 DB 135 SVHGPPIVELAVALFOTGKLYLLECLSGGELFTLHREBGFLEBDTACPYLAITLALGH 194  
 QY 198 LHSOGIITRDLPENITLSSGCHITLTPGLCKESIHEGAVTHTECGTIEYAPPELVAS 257  
 DB 195 LHSOGIITRDLPENITLSSGCHITLTPGLCKESIHEGAVTHTECGTIEYAPPELVAS 254  
 QY 258 GNNRAVDMWSLGAALYDMLTJGSPPTAENRKKTMKXIRGKALPPLYTPDARDLVKKFL 317  
 DB 255 GNNRAVDMWSLGAALYDMLTJGSPPTAENRKKTMKXIRGKALPPLYTPDARDLVKKFL 314  
 QY 318 KNPSPQRIQGGPGDAADVQRHFFRHMNDLLAMRVDPFRPCLQSEEDVSQDFTRFTR 377

DB 315 KNPSPQRIQGGPGDAADVQRHFFRHMNDLLAMRVDPFRPCLQSEEDVSQDFTRFTR 374  
 QY 378 QTPVSDPDDTLASANQAFGLFTYVAPSVLDSIKGFSFOKLSPRRLNSSPR 432  
 DB 375 QTPVSDPDDTLASANQAFGLFTYVAPSVLDSIKGFSFOKLSPRRLNSSPR 424

## RESULT 7

US-09-430-564-12  
 ; Sequence 12, Application US/09430564  
 ; Patent No. 6372467  
 ; GENERAL INFORMATION:  
 ; APPLICANT: John Blenis  
 ; APPLICANT: Kay K. Lee-Fruman  
 ; APPLICANT: Calvin J. Kuo  
 ; TITLE OF INVENTION: P54SK AND P85SK GENES, PROTEINS,  
 ; FILE REFERENCE: 00246/506002  
 ; CURRENT APPLICATION NUMBER: US/09/430,564  
 ; CURRENT FILING DATE: 1998-10-29  
 ; PRIOR APPLICATION NUMBER: 60/106,141  
 ; PRIOR FILING DATE: 1998-10-29  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 12  
 ; LENGTH: 268  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-430-564-12

Query Match 54.1%; Score 1415; DB 4; Length 268;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-110;  
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 HCEFLRLVTLGKGYGVQVRKVQGTNGLKIYAMKVLRAKIYRANADTAHTRAEINLIE 137  
 DB 1 HCEFLRLVTLGKGYGVQVRKVQGTNGLKIYAMKVLRAKIYRANADTAHTRAEINLIE 60  
 QY 138 SVHGPPIVELAVALFOTGKLYLLECLSGGELFTLHREBGFLEBDTACPYLAITLALGH 197  
 DB 61 SVHGPPIVELAVALFOTGKLYLLECLSGGELFTLHREBGFLEBDTACPYLAITLALGH 120  
 QY 198 LHSOGIITRDLPENITLSSGCHITLTPGLCKESIHEGAVTHTECGTIEYAPPELVAS 257  
 DB 121 LHSOGIITRDLPENITLSSGCHITLTPGLCKESIHEGAVTHTECGTIEYAPPELVAS 180  
 QY 258 GNNRAVDMWSLGAALYDMLTJGSPPTAENRKKTMKXIRGKALPPLYTPDARDLVKKFL 317  
 DB 181 GNNRAVDMWSLGAALYDMLTJGSPPTAENRKKTMKXIRGKALPPLYTPDARDLVKKFL 240  
 QY 318 KNPSPQRIQGGPGDAADVQRHFFRHMN 345  
 DB 241 KNPSPQRIQGGPGDAADVQRHFFRHMN 268

## RESULT 8

US-08-749-902-3  
 ; Sequence 3, Application US/08749902  
 ; Patent No. 5985635  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bandman, Olga  
 ; APPLICANT: Goli, Surya K.  
 ; APPLICANT: Hillman, Jennifer L.  
 ; TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: US

ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION NUMBER: 60/105,141  
APPLICATION NUMBER: US/08/749,902  
FILING DATE: Filed Herewith  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0150 US  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 495 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: Consensus  
US-08-749-902-3

Query Match 51.0%; Score 1385.5; DB 2; Length 495;  
Best Local Similarity 61.7%; Pred. No. 5.3e-107;  
Matches 282; Conservative 39; Mismatches 75; Indels 61; Gaps 9;

QY 86 LGKGGVGVKVRKVGQTNL--GKIYAMKYLK-----KAKIYRNADTAHTAERNILE 137  
DB 43 LGBAHARVQTC-----INLITSOEYXVXIIIFPKGHINRSVFEVEMLYQCQGHNVLE 97  
QY 138 SVKHPIVELAYAFQTKGLYLILKLSGSELFTHLERBGI FLEDTACFYLAETITLALGH 197  
DB 98 LIEF-----FEEDRFYLVFEKVRGGSILSHIKRRHPHELEASVVVQVVASALDF 148  
QY 198 LHSQGIYRDLKRNIMLSSQGH---IKLDFGLCKESIHGAVTH-----TFQGTIR 247  
DB 149 LHNKGAHARDLKRNILCERNPNVSPVKIDFDLGGSGIKLNGCSPISRELLTFFQGSAB 208  
QY 248 YMAPEI-----LVRSGRNRAVD--WMS---LGALMYDNLG 278  
DB 209 YMAPEVVEAESEASITDKKCDLMSGLVILYILSGIPPPVGRNMQRLRGLPTMYMLTG 268  
QY 279 SPPTAENRRTKTKMDKIIIRGKLALPPYLTDPADLVKKFLKRNPSQRIIGGPGDADVQRH 338  
DB 269 SPPTAENRRTKTKMDKIIIRGKLALPPYLTDPADLVKKFLKRNPSQRIIGGPGDADVQRH 328  
QY 339 PPRHNMNDLMLARVDPPEPRPCLOSEBEVSQFDTFRTPROTVPDSDDTLASRANQAF 398  
DB 329 PPRHNMNDLMLARVDPPEPRPCLOSEBEVSQFDTFRTPROTVPDSDDTLASRANQAF 388  
QY 399 GFTYVAPSVLDSIKEGFSQPKLRSRRRLNSSRPVSPKFSFGFRSPSPSPSPSPSPSP 458  
DB 389 GFTYVAPSVLDSIKEGFSQPKLRSRRRLNSSRPVSPKFSFGFRSPSPSPSPSPSPSP 448  
QY 459 PLPELPPPPPTTAPLPIRPPSGTKSKKGRGRGR 495  
DB 449 PLPELPPPPPTTAPLPIRPPSGTKSKKGRGRGR 485

RESULT 9  
US-09-430-564-6  
Sequence 6, Application US/09430564  
Patent No. 6372467  
GENERAL INFORMATION:  
APPLICANT: John Blenis  
APPLICANT: Kay K. Lee-Fruman

APPLICANT: Calvin J. Kuo  
TITLE OF INVENTION: P54S6K AND P85S6K GENES, PROTEINS,  
FILE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS  
FILE REFERENCE: 00246/506002  
CURRENT APPLICATION NUMBER: US/09/430,564  
CURRENT FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: 60/105,141  
PRIOR FILING DATE: 1998-10-29  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 258  
TYPE: PRP  
ORGANISM: Homo sapiens  
US-09-430-564-6

Query Match 51.8%; Score 1354; DB 4; Length 258;  
Best Local Similarity 100.0%; Pred. No. 9.2e-105;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 HCEELLRVLAGKGGYGVQVRKVGQTNLKGKIYAMKYLKRAKIVRNADTAHTAERNILE 137  
DB 1 HCEELLRVLAGKGGYGVQVRKVGQTNLKGKIYAMKYLKRAKIVRNADTAHTAERNILE 60  
QY 138 SVKHPIVELAYAFQTKGLYLILKLSGSELFTHLERBGI FLEDTACFYLAETITLALGH 197  
DB 61 SVKHPIVELAYAFQTKGLYLILKLSGSELFTHLERBGI FLEDTACFYLAETITLALGH 120  
QY 198 LHSQGIYRDLKRNIMLSSQGHIIKLTDFGLCKESIHGAVTHTFQGTIRYMAPEILVRS 257  
DB 121 LHSQGIYRDLKRNIMLSSQGHIIKLTDFGLCKESIHGAVTHTFQGTIRYMAPEILVRS 180  
QY 258 GHNRAVDWMSLGAIAWDMLTGSPPTAENRRTKTKMDKIIIRGKLALPPYLTDPADLVKKFL 317  
DB 181 GHNRAVDWMSLGAIAWDMLTGSPPTAENRRTKTKMDKIIIRGKLALPPYLTDPADLVKKFL 240  
QY 318 KNPSSQRIIGGPGDADV 335  
DB 241 KNPSSQRIIGGPGDADV 258

RESULT 10  
US-09-031-295-2  
Sequence 2, Application US/09031295  
Patent No. 6326181  
GENERAL INFORMATION:  
APPLICANT: LANG, Florian  
TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/031,295  
FILING DATE: 26-FEB-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 197-08-173.8  
FILING DATE: 28-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Sandercock, Colin G.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 058315/0123

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 431 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-031-295-2

Query Match 30.9%; Score 806.5; DB 4; Length 431;  
Best Local Similarity 44.3%; Pred. No. 5.7e-59;  
Matches 172; Conservative 66; Mismatches 111; Indels 39; Gaps 12;

QY 33 EPELSPADACPLAEIRAAAGLEPVGHVEVELTETSVNNGPERIGPHC---PELLRVLCX 88  
DB 65 EPELNNANPSP-----PPSPSQ-----INLGSS-NPHAKPSDFHFLKVIKX 106  
QY 89 GGKGVQVQR-KVQGTNLGKIYAMKYLAKKIVRNADTAETRAERNI-LESYKSPFIYE 146  
DB 107 GSGKVLARHKAEEV---FYAVKVLQKALIKR-KBKHMSEERNVILKNVKEPFLVG 161  
QY 147 IAAVPTQSGKLYLIECLSGSELFTLHREGIFLEDYACFYLAETTLALGHLHSGGIYR 206  
DB 162 LHSFQPADKLYFLVDYINGELFYHLQRECFLEPRARFYAEIASALGYLHSLNIYR 221  
QY 207 DLRPNIMLSSQGHKLTDFGCKESIHGAVTHFCGTEYNAPEILVRSGHNRADVW 266  
DB 222 DLRPNILDSQGHVLTDFGCKENIENHSTSTFCGTEYNAPEILVRSKHQPDRTYDW 281  
QY 267 SIGALMYDMLTGSPPFTAEARNKKTMDKILRGKALPPYLTDPADLVKFLKRNPSQRI 326  
DB 282 CLGAVLYEMLYGPPFYSRNTAEMTDNINKPLQKPNITNSARHLBGLQKDTKRL- 340  
QY 327 GSGGDAADVQRHPPFRHNMMDLLAMRVDPFRPCLOSEEDVSQPTFRQTPV----- 381  
DB 341 GAQDPMETKSHVFFSLINMDLLINKKITPPENPVSGPMDLRHDPDEFER-PVPNSIG 399  
QY 382 DSPDD---TALSESANOAFLETTYAPS 406  
DB 400 KSPDSVLTASVKEAAEAFLEGSYAPPT 427

RESULT 11  
US-08-712-709-5  
Sequence 5, Application US/08712709  
Patent No. 563780  
GENERAL INFORMATION:  
APPLICANT: Au-Young, Janice  
APPLICANT: Guegler, Karl J.  
APPLICANT: Hawkins, Phillip R.  
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/712,709  
FILING DATE: Filed Hereewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy U  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 431 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE: Consensus  
US-08-712-709-5

Query Match 30.7%; Score 802.5; DB 2; Length 431;  
Best Local Similarity 44.3%; Pred. No. 1.2e-58;  
Matches 172; Conservative 65; Mismatches 112; Indels 39; Gaps 12;

QY 33 EPELSPADACPLAEIRAAAGLEPVGHVEVELTETSVNNGPERIGPHC---PELLRVLCX 88  
DB 65 EPELNNANPSP-----PPSPSQ-----INLGSS-NPHAKPSDFHFLKVIKX 106  
QY 89 GGKGVQVQR-KVQGTNLGKIYAMKYLAKKIVRNADTAETRAERNI-LESYKSPFIYE 146  
DB 107 GSGKVLARHKAEEV---FYAVKVLQKALIKR-KBKHMSEERNVILKNVKEPFLVG 161  
QY 147 IAAVPTQSGKLYLIECLSGSELFTLHREGIFLEDYACFYLAETTLALGHLHSGGIYR 206  
DB 162 LHSFQPADKLYFLVDYINGELFYHLQRECFLEPRARFYAEIASALGYLHSLNIYR 221  
QY 207 DLRPNIMLSSQGHKLTDFGCKESIHGAVTHFCGTEYNAPEILVRSGHNRADVW 266  
DB 222 DLRPNILDSQGHVLTDFGCKENIENHSTSTFCGTEYNAPEILVRSKHQPDRTYDW 281  
QY 267 SIGALMYDMLTGSPPFTAEARNKKTMDKILRGKALPPYLTDPADLVKFLKRNPSQRI 326  
DB 282 CLGAVLYEMLYGPPFYSRNTAEMTDNINKPLQKPNITNSARHLBGLQKDTKRL- 340  
QY 327 GSGGDAADVQRHPPFRHNMMDLLAMRVDPFRPCLOSEEDVSQPTFRQTPV----- 381  
DB 341 GAQDPMETKSHVFFSLINMDLLINKKITPPENPVSGPMDLRHDPDEFER-PVPNSIG 399  
QY 382 DSPDD---TALSESANOAFLETTYAPS 406  
DB 400 KSPDSVLTASVKEAAEAFLEGSYAPPT 427

RESULT 12  
US-09-111-444-5  
Sequence 5, Application US/09111444  
Patent No. 6045792  
GENERAL INFORMATION:  
APPLICANT: Au-Young, Janice  
APPLICANT: Guegler, Karl J.  
APPLICANT: Hawkins, Phillip R.  
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/111,444  
FILING DATE:



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/712,709  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0118 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 431 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE: Consensus  
US-09-111-444-5

Query Match 30.7%; Score 802.5; DB 3; Length 431;  
Best Local Similarity 44.3%; Pred. No. 1.2e-58;  
Matches 172; Conservative 65; Mismatches 112; Indels 39; Gaps 12;

QY 33 EPELSPADACPLAEALRAAGLEPVGHVEVELTETSVMVPERIGPHC---FELLRLVLRK 88  
DB 65 EPELMMANPSP-----PPSPSQ-----INLGPSS-NPRAKPSDFHFLVLRK 106  
QY 89 GGYKVFQVR-KVQGTNLGIYAMKVLRAKIVNADTAHTRAERNI-LESYKHPPIVE 146  
DB 107 GSFQKVLARHRAEVR---FYAVVLOKKAALKK-KEKHIMSEBVLKKNVHPFLVG 161  
QY 147 LAAVFGTGKLYLIECLSGSELFTHLEREGIFLEDTACFYLAETTLAIGHLSQCIYR 206  
DB 162 LHPSFQTAOKLYFVLDYINGSELFTHLQRERCFLEPRASVAAEIASALGYHSLNIVYR 221  
QY 207 DLKPEINIMSSQGHKILTDGFCCKESIHEGAVTHTFCCGTEYMAPEILVRSNGHRAVDW 266  
DB 222 DLKPEINILDSQGHIVLTDGFCCKENIENSTSTFCGTEYLAPEVLHKOYDRIVDW 281  
QY 267 SLGALMYDNLTGSPPTAENRKKTKMDKIIRGKLALPYLTPDARDLVKKFLKRNPSQRIQ 326  
DB 282 CGAVLYEMLYGILPFFYSRNTAEMTDNINLKEPLQKPNITNSARHLIEGLQKDRYKRL- 340  
QY 327 GGPDAADVQRRHPPFRHNMWDLLAMRVDPFRPCLOSEEDVSGQDTRFRTPQPV----- 381  
DB 341 GAKDDPMEIKSHVFPFLINWDDLINCKITPPENPNVSGENDLHFPDEFTER-PVPNSIG 399  
QY 382 DSPDD---TALSASANQAFIGFTYVAPS 406  
DB 400 KSPDSVLTASVKEAAEAFIGFSYAPPT 427

RESULT 13  
US-09-541-228-5  
Sequence 5, Application US/09541228  
Patent No. 6232077  
GENERAL INFORMATION:  
APPLICANT: Au-Young, Janice  
APPLICANT: Guegler, Karl J.  
APPLICANT: Hawkins, Phillip R.  
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/541,228  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/712,709  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0118 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 431 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE: Consensus  
US-09-541-228-5

Query Match 30.7%; Score 802.5; DB 3; Length 431;  
Best Local Similarity 44.3%; Pred. No. 1.2e-58;  
Matches 172; Conservative 65; Mismatches 112; Indels 39; Gaps 12;

QY 33 EPELSPADACPLAEALRAAGLEPVGHVEVELTETSVMVPERIGPHC---FELLRLVLRK 88  
DB 65 EPELMMANPSP-----PPSPSQ-----INLGPSS-NPRAKPSDFHFLVLRK 106  
QY 89 GGYKVFQVR-KVQGTNLGIYAMKVLRAKIVNADTAHTRAERNI-LESYKHPPIVE 146  
DB 107 GSFQKVLARHRAEVR---FYAVVLOKKAALKK-KEKHIMSEBVLKKNVHPFLVG 161  
QY 147 LAAVFGTGKLYLIECLSGSELFTHLEREGIFLEDTACFYLAETTLAIGHLSQCIYR 206  
DB 162 LHPSFQTAOKLYFVLDYINGSELFTHLQRERCFLEPRASVAAEIASALGYHSLNIVYR 221  
QY 207 DLKPEINIMSSQGHKILTDGFCCKESIHEGAVTHTFCCGTEYMAPEILVRSNGHRAVDW 266  
DB 222 DLKPEINILDSQGHIVLTDGFCCKENIENSTSTFCGTEYLAPEVLHKOYDRIVDW 281  
QY 267 SLGALMYDNLTGSPPTAENRKKTKMDKIIRGKLALPYLTPDARDLVKKFLKRNPSQRIQ 326  
DB 282 CGAVLYEMLYGILPFFYSRNTAEMTDNINLKEPLQKPNITNSARHLIEGLQKDRYKRL- 340  
QY 327 GGPDAADVQRRHPPFRHNMWDLLAMRVDPFRPCLOSEEDVSGQDTRFRTPQPV----- 381  
DB 341 GAKDDPMEIKSHVFPFLINWDDLINCKITPPENPNVSGENDLHFPDEFTER-PVPNSIG 399  
QY 382 DSPDD---TALSASANQAFIGFTYVAPS 406  
DB 400 KSPDSVLTASVKEAAEAFIGFSYAPPT 427

RESULT 14  
US-08-712-709-9  
Sequence 9, Application US/08712709  
Patent No. 5863780  
GENERAL INFORMATION:  
APPLICANT: Au-Young, Janice  
APPLICANT: Guegler, Karl J.  
APPLICANT: Hawkins, Phillip R.  
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:

ADDRESSES: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: U.S.  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/712,709  
 FILING DATE: Filed Herewith  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0118 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 430 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 294637  
 US-08-712-709-9

Query Match 30.3%; Score 791; DB 2; Length 430;  
 Best Local Similarity 44.4%; Pred. No. 1,1e-57;  
 Matches 174; Conservative 64; Mismatches 112; Indels 42; Gaps 14;  
 DB 65 EPELSPADACPLAEPLAAGLEPVGHYEVEVLTETSVNNGPRIGPHC---FELLRLVGLK 88  
 33 EPELSPADACPLAEPLAAGLEPVGHYEVEVLTETSVNNGPRIGPHC---FELLRLVGLK 88  
 65 EPELSPADACPLAEPLAAGLEPVGHYEVEVLTETSVNNGPRIGPHC---FELLRLVGLK 106  
 DB 89 GGYGVKFOVR-KVQGTNLGKIYAMKVIKAKIVRNKOTAHTRAERNT-LESVKHPFIYE 146  
 107 GSGFGVLLARHKAEEA---FYAVVYLOKKAILEK-KEEKIMSERVNLKXVKAPFLVG 161  
 DB 147 LAYAFOTGKLYLILECISGSEFLTEERGIPLBDTACPYLAETITLALGHLISGIIYR 206  
 162 LHPSTQADKLYFVDIYNGSELPHYLQREKCFLEPRARFAAEIASLGYHSLNIYTR 221  
 DB 207 DLRPENIMLSGGHILKIDFGICSEIHGCAVHTTFCGTIYMAPEIIVRSGENRVDWM 266  
 222 DLRPENIMLSGGHILKIDFGICSEIHGCAVHTTFCGTIYMAPEIIVRSGENRVDWM 281  
 DB 267 SIGALMYDMLTSSPPPTAENRKKTMKTIIRGKALPPYLTPDARDLVKKPIKRNPSQIRG 326  
 282 CLGAVLYEMLYGLPPFYSRNTAEMYNILAKPIQL-KNITNSAKHLBGLQOKTKRL- 339  
 DB 327 GSGFGADAVQRRHPPFRHNMWDLAMRVDPPEPRCLOSSEDDVSQDTRFTROTVD--- 382  
 340 GAKDQFWEIKSHIFFSLINMDDLINKKITPPFNPNVSGPSDLRHPDEPTEE-PVPSISIG 398  
 DB 383 -SPDD---TALSSEANOAFIGETVAPSVYDS 410  
 399 RSPDSILVTASVKEAAEAFIGETVAPP--WDS 428

RESULT 15  
 US-09-111-444-9  
 Sequence 9, Application US/09111444  
 Patent No. 6045792  
 GENERAL INFORMATION:  
 APPLICANT: Au-Young, Janice  
 APPLICANT: Guegler, Karl J.

APPLICANT: Hawkins, Phillip R.  
 TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSES: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: U.S.  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/111,444  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/712,709  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0118 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 430 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 294637  
 US-09-111-444-9

Query Match 30.3%; Score 791; DB 3; Length 430;  
 Best Local Similarity 44.4%; Pred. No. 1,1e-57;  
 Matches 174; Conservative 64; Mismatches 112; Indels 42; Gaps 14;  
 DB 33 EPELSPADACPLAEPLAAGLEPVGHYEVEVLTETSVNNGPRIGPHC---FELLRLVGLK 88  
 65 EPELSPADACPLAEPLAAGLEPVGHYEVEVLTETSVNNGPRIGPHC---FELLRLVGLK 106  
 DB 89 GGYGVKFOVR-KVQGTNLGKIYAMKVIKAKIVRNKOTAHTRAERNT-LESVKHPFIYE 146  
 107 GSGFGVLLARHKAEEA---FYAVVYLOKKAILEK-KEEKIMSERVNLKXVKAPFLVG 161  
 DB 147 LAYAFOTGKLYLILECISGSEFLTEERGIPLBDTACPYLAETITLALGHLISGIIYR 206  
 162 LHPSTQADKLYFVDIYNGSELPHYLQREKCFLEPRARFAAEIASLGYHSLNIYTR 221  
 DB 207 DLRPENIMLSGGHILKIDFGICSEIHGCAVHTTFCGTIYMAPEIIVRSGENRVDWM 266  
 222 DLRPENIMLSGGHILKIDFGICSEIHGCAVHTTFCGTIYMAPEIIVRSGENRVDWM 281  
 DB 267 SIGALMYDMLTSSPPPTAENRKKTMKTIIRGKALPPYLTPDARDLVKKPIKRNPSQIRG 326  
 282 CLGAVLYEMLYGLPPFYSRNTAEMYNILAKPIQL-KNITNSAKHLBGLQOKTKRL- 339  
 DB 327 GSGFGADAVQRRHPPFRHNMWDLAMRVDPPEPRCLOSSEDDVSQDTRFTROTVD--- 382  
 340 GAKDQFWEIKSHIFFSLINMDDLINKKITPPFNPNVSGPSDLRHPDEPTEE-PVPSISIG 398  
 DB 383 -SPDD---TALSSEANOAFIGETVAPSVYDS 410  
 399 RSPDSILVTASVKEAAEAFIGETVAPP--WDS 428

Wed Jul 7 12:18:44 2004

us-09-762-258-2.ra1

Page 9

Search completed: June 30, 2004, 17:15:19  
Job time : 25 secs

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QY	449	GACACAGCACACACAGGGCTGAGCGGAAACATTTGAGCTCACTGAAGACACCCCTTAT	508
Db	369	GACACAGCACACACAGGGCTGAGCGGAAACATTTGAGCTCACTGAAGACACCCCTTAT	428
QY	509	GTGAAACTGGCCTATTCCTTCCAGACTGTGTGGAAACTTCACTCACTCTTGAATGCTTC	568
Db	429	GTGAAACTGGCCTATTCCTTCCAGACTGTGTGGAAACTTCACTCACTCTTGAATGCTTC	488
QY	569	AGTGTGTGGAGACTCTTTCAGCATCTGAGAGCAGAGGGCATCTTCTGTGAAGATACGGCC	628
Db	489	AGTGTGTGGAGACTCTTTCAGCATCTGAGAGCAGAGGGCATCTTCTGTGAAGATACGGCC	548
QY	629	TGCTTCTACCTGGCTGAGATCAAGCTGGCTGGGGCATCTTCCACTCCAGGGCATCATC	688
Db	549	TGCTTCTACCTGGCTGAGATCAAGCTGGCTGGGGCATCTTCCACTCCAGGGCATCATC	608
QY	689	TACCGGGACCTCAAGCGCCAGAAACATCATGCTCAGAGCGCAGGGCCACATCAACTGACCC	748
Db	609	TACCGGGACCTCAAGCGCCAGAAACATCATGCTCAGAGCGCAGGGCCACATCAACTGACCC	668
QY	749	GACTTTGGACTCTGACAGAGATCTATCCATGAGGGCGCCGTCACTCAACTCTTGGCGGC	808
Db	669	GACTTTGGACTCTGACAGAGATCTATCCATGAGGGCGCCGTCACTCAACTCTTGGCGGC	728
QY	809	ACCATTGAGTACATGAGCCCTGAGATTCTGTGTGCGCAGTGGCCACAAACCGAGCTGTGAC	868
Db	729	ACCATTGAGTACATGAGCCCTGAGATTCTGTGTGCGCAGTGGCCACAAACCGAGCTGTGAC	788
QY	869	TGTTGGAAGCTTGGGGGCTCTGATGTACGACATGTCTCATGTGATCCCGGCTTTACCGCA	928
Db	789	TGTTGGAAGCTTGGGGGCTCTGATGTACGACATGTCTCATGTGATCCCGGCTTTACCGCA	848
QY	929	GAGAACCGGAGAAACCATGTGATAGATCATCAGGGGCAAGCTGGCATGCGCCCTTAC	988
Db	849	GAGAACCGGAGAAACCATGTGATAGATCATCAGGGGCAAGCTGGCATGCGCCCTTAC	908
QY	989	CTCACTCCAGATGCTCCCGGAGCCTTGTCAAAAAGTTTCTGAACCGAATCCAGCCAGCGG	1048
Db	909	CTCACTCCAGATGCTCCCGGAGCCTTGTCAAAAAGTTTCTGAACCGAATCCAGCCAGCGG	968
QY	1049	ATTGGGGGGTGGCCAGGGGGATCTGTGTGTGAGAGACATCCCTTTTCCGGGACATG	1108
Db	969	ATTGGGGGGTGGCCAGGGGGATCTGTGTGTGAGAGACATCCCTTTTCCGGGACATG	1028
QY	1109	AATTGGGACGACCTTCTGACCTGCGGTGTGAACCCCTTTTCAAGCCCTGTCTGTGACATCA	1168
Db	1029	AATTGGGACGACCTTCTGACCTGCGGTGTGTGAACCCCTTTTCAAGCCCTGTCTGTGACATCA	1088
QY	1169	GAGAGAGAGGTGAGCAGATTTATATACCGCTTCAACGCGCAGAGCGCCGGTGGACATGCTCT	1228
Db	1089	GAGAGAGAGGTGAGCAGATTTATATACCGCTTCAACGCGCAGAGCGCCGGTGGACATGCTCT	1148
QY	1229	GATGACACAGCCTCTCAGCGAGATGTCCAAACGAGCCTTCTGTGGCTTCAATAGTGTGCG	1288
Db	1149	GATGACACAGCCTCTCAGCGAGATGTCCAAACGAGCCTTCTGTGGCTTCAATAGTGTGCG	1208
QY	1289	CCGTGTGTCTGTGACGATCAAGAGAGGGCTTCTCTTCCAGACCCAAAGCTAGGCTCAACC	1348
Db	1209	CCGTGTGTCTGTGACGATCAAGAGAGGGCTTCTCTTCCAGACCCAAAGCTAGGCTCAACC	1268
QY	1349	AGGGGCTCTCAAGTAAAGCTCCCGGGTCCCTCTCAAGCCTCCCTCAAGTTCTCCCTTTTGA	1408
Db	1269	AGGGGCTCTCAAGTAAAGCTCCCGGGTCCCTCTCAAGCCTCCCTCAAGTTCTCCCTTTTGA	1328
QY	1409	GGGTTTCCGACCGCCAGCCTGCGCGAGCCACAGGAGCTAACCTTACTCTCACTCTG	1468
Db	1329	GGGTTTCCGACCGCCAGCCTGCGCGAGCCACAGGAGCTAACCTTACTCTCACTCTG	1388
QY	1469	CCACCGCGCGCGCCTTGCACACCGCGCTCTCTCCATCCGTCCCTCTCAAGGACACAG	1528
Db	1389	CCACCGCGCGCGCCTTGCACACCGCGCTCTCTCCATCCGTCCCTCTCAAGGACACAG	1448

QY 1559 AAGTCGCAAGAGGCGCCGTGGCCGTCCAGAGGCGCTAGGAAGCCGGGTGGGCTGAGGGTAG 1568

Db 1449 AAGTCGCAAGAGGCGCCGTGGCCGTCCAGAGGCGCTAGGAAGCCGGGTGGGCTGAGGGTAG 1508

QY 1589 CCCTTGAGCCCTGTCCCTCGCGCGCTGTGAGAGCAGCAAGACCCTGGGCCAGTTCCAGAGAC 1648

Db 1509 CCCCTGAGCCCTGTCCCTCGCGCGCTGTGAGAGCAGCAAGACCCTGGGCCAGTTCCAGAGAC 1568

QY 1649 CTGGGGGTGTGTCTGGGGGGGTGGGGGTGTGAGAGCGCTATGAAAGATGTGTCTGCTGGGGCA 1708

Db 1569 CTGGGGGTGTGTCTGGGGGGGTGGGGGTGTGAGAGCGCTATGAAAGATGTGTCTGCTGGGGCA 1628

QY 1709 GCTGTGCCCTCGAATCATGGGCAAGAGGCGCGCCGCCACACCCCGCGCTCAACTGCTC 1768

Db 1629 GCTGTGCCCTCGAATCATGGGCAAGAGGCGCGCGCCGCCACACCCCGCGCTCAACTGCTC 1688

QY 1769 CCGTGGAAAGATTAAAGGCGTGAATCATGAAAAAAGAAAAA 1812

Db 1689 CCGTGGAAAGATTAAAGGCGTGAATCATGAAAAAAGAAAAA 1732

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1      RESULT 2
2      US-08-966-316-10
3      ; Sequence 10, Application US/08966316
4      ; Patent No. 5932445
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Lal, Preeti
7      ; APPLICANT: Au-Young, Janice
8      ; APPLICANT: Reddy, Roopa
9      ; APPLICANT: Murry, Lynn B.
10     ; APPLICANT: Mathur, Preete
11     ; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
12     ; NUMBER OF SEQUENCES: 18
13     ; CORRESPONDENCE ADDRESS:
14     ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
15     ; STREET: 3174 Porter Drive
16     ; CITY: Palo Alto
17     ; STATE: CA
18     ; COUNTRY: USA
19     ; ZIP: 94304
20     ; COMPUTER READABLE FORM:
21     ; MEDIUM TYPE: Diskette
22     ; COMPUTER: IBM Compatible
23     ; OPERATING SYSTEM: DOS
24     ; SOFTWARE: FASTSQ for Windows Version 2.0
25     ; CURRENT APPLICATION DATA:
26     ; APPLICATION NUMBER: US/08/966,316
27     ; FILING DATE: Herewith
28     ; CLASSIFICATION: 435
29     ; PRIOR APPLICATION DATA:
30     ; APPLICATION NUMBER:
31     ; FILING DATE:
32     ; ATTORNEY/AGENT INFORMATION:
33     ; NAME: Billings, Lucy J.
34     ; REGISTRATION NUMBER: 36,749
35     ; REFERENCE/DOCKET NUMBER: PF-0424 US
36     ; TELECOMMUNICATION INFORMATION:
37     ; TELEPHONE: 650-855-0555
38     ; TELEFAX: 650-845-4166
39     ; TELEX:
40     ; INFORMATION FOR SEQ ID NO: 10:
41     ; SEQUENCE CHARACTERISTICS:
42     ; LENGTH: 1637 base pairs
43     ; TYPE: nucleic acid
44     ; STRANDEDNESS: single
45     ; TOPOLOGY: linear
46     ; IMMEDIATE SOURCE:
47     ; LIBRARY: SKINBT01
48     ; CLONE: 1869688
49     ; US-08-966-316-10
50
51 Query Match 60.8%; Score 1104.4; DB 2; Length 1637;
52 Best Local Similarity 98.8%; Pctd. No. 4; 5e-249;

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Db      1048  GGGTGGCCCAAGGGATGCTGCTGATGTCAGAGACATCCCTTTTTCGGCAGATGAATTG 1107
Qy      1114  GAGAGACCTTCTGCGCTGCGGTGGAACCCCTTTTCAAGCCCTGTCTGAGTCAGAGGA 1173
Db      1108  GAGAGACCTTCTGCGCTGCGGTGGAACCCCTTTTCAAGCCCTGTCTGAGTCAGAGGA 1167
Qy      1174  GAGAGAGCAGATTGATACCGCTTCAAGAGGAGAGCGCGGTGAGACATCTGATGA 1233
Db      1168  GAGAGAGCAGATTGATACCGCTTCAAGAGGAGAGCGCGGTGAGACATCTGATGA 1227
Qy      1234  CACAGCCCTCAGCGAGAGTCCCAACAGGCTTCTGAGGCTTCACTAGTCAGCGCGT 1293
Db      1228  CACAGCCCTCAGCGAGAGTCCCAACAGGCTTCTGAGGCTTCACTAGTCAGCGCGT 1287
Qy      1294  TGTCTGAGACAGATCAAGAGAGGCTTCTCTTCCAGCCCAAGCTGCGTCAACCCAGCG 1353
Db      1288  TGTCTGAGACAGATCAAGAGAGGCTTCTCTTCCAGCCCAAGCTGCGTCAACCCAGCG 1347
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Db      1348  CTTCAACAGTAGCCCCCGGCTCCCGTCAAGCCCTCAAGTTCTCCCTTTTGAAGGATT 1407
Qy      1414  TCGGCCCCAGCCCAAGCCTGCGGAGCCCAAGAGCTTACTTACTTCACTCTGCAACC 1473
Db      1408  TCGGCCCCAGCCCAAGCCTGCGGAGCCCAAGAGCTTACTTACTTCACTCTGCAACC 1467
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Db      1468  GCGCGCGCCCTCGACCAACGCGCCCTCTGCCATCCGTCGCCCTCTCAAGGAGCAAGAATG 1527
Qy      1534  CAAGAGGGCGCTGAGGCGTCCAGGCGCTGAGAGGCTGAGGCTGAGGCTGAGGCTT 1593
Db      1528  CAAGAGGGCGCTGAGGCGTCCAGGCGCTGAGAGGCTGAGGCTGAGGCTGAGGCTT 1586
Qy      1594  GAGCCCTGTCCCTGCGGCTGT 1614
Db      1587  GAGCCCTGTCCCTGCGGCTGT 1607

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RESULT 4  
 US-09-016-434-126  
 ; Sequence 126, Application US/09016434  
 ; Patent No. 6500938  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Janice Au-Young  
 ; APPLICANT: Jeffrey J. Sellhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1490  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/016,434  
 ; FILING DATE: HERewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:

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; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLINFET02
; CLONE: 1309709
; US-09-016-434-126

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Query Match 39.6%; Score 720; DB 4; Length 1607;  
 Best Local Similarity 99.1%; Pred. No. 3,7e-159;  
 Matches 734; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Qy      874  GAGCCTGGGCGCTGATGTAAGACATGCTCACTGATGATCGCGCCCTTACCGCAGAGA 933
Db      868  GCGGCTGGGAGCCGCTGATGTAAGACATGCTCACTGATGATCGCGCCCTTACCGCAGAGA 927
Qy      934  CCGGAGAAACCATGATGTAAGATCATAGGCGCAAGCTGGCACTGCCCTTACTCTAC 993
Db      928  CCGGAGAAACCATGATGTAAGATCATAGGCGCAAGCTGGCACTGCCCTTACTCTAC 987
Qy      994  CCGGAGAAACCATGATGTAAGATCATAGGCGCAAGCTGGCACTGCCCTTACTCTAC 1053
Db      988  CCGGAGAAACCATGATGTAAGATCATAGGCGCAAGCTGGCACTGCCCTTACTCTAC 1047
Qy      1054  GGGTGGCCCAAGGGATGCTGCTGATGTCAGAGACATCCCTTTTTCGGCAGATGAATTG 1113
Db      1048  GGGTGGCCCAAGGGATGCTGCTGATGTCAGAGACATCCCTTTTTCGGCAGATGAATTG 1107
Qy      1114  GAGAGACCTTCTGCGCTGCGGTGGAACCCCTTTTCAAGCCCTGTCTGAGTCAGAGGA 1173
Db      1108  GAGAGACCTTCTGCGCTGCGGTGGAACCCCTTTTCAAGCCCTGTCTGAGTCAGAGGA 1167
Qy      1174  GAGAGAGCAGATTGATACCGCTTCAAGAGGAGAGCGCGGTGAGACATCTGATGA 1233
Db      1168  GAGAGAGCAGATTGATACCGCTTCAAGAGGAGAGCGCGGTGAGACATCTGATGA 1227
Qy      1234  CACAGCCCTCAGCGAGAGTCCCAACAGGCTTCTGAGGCTTCACTAGTCAGCGCGT 1293
Db      1228  CACAGCCCTCAGCGAGAGTCCCAACAGGCTTCTGAGGCTTCACTAGTCAGCGCGT 1287
Qy      1294  TGTCTGAGACAGATCAAGAGAGGCTTCTCTTCCAGCCCAAGCTGCGTCAACCCAGCG 1353
Db      1288  TGTCTGAGACAGATCAAGAGAGGCTTCTCTTCCAGCCCAAGCTGCGTCAACCCAGCG 1347
Qy      1354  CTTCAACAGTAGCCCCCGGCTCCCGTCAAGCCCTCAAGTTCTCCCTTTTGAAGGATT 1413
Db      1348  CTTCAACAGTAGCCCCCGGCTCCCGTCAAGCCCTCAAGTTCTCCCTTTTGAAGGATT 1407
Qy      1414  TCGGCCCCAGCCCAAGCCTGCGGAGCCCAAGAGCTTACTTACTTCACTCTGCAACC 1473
Db      1408  TCGGCCCCAGCCCAAGCCTGCGGAGCCCAAGAGCTTACTTACTTCACTCTGCAACC 1467
Qy      1474  GCGCGCGCCCTCGACCAACGCGCCCTCTGCCATCCGTCGCCCTCTCAAGGAGCAAGAATG 1533
Db      1468  GCGCGCGCCCTCGACCAACGCGCCCTCTGCCATCCGTCGCCCTCTCAAGGAGCAAGAATG 1527
Qy      1534  CAAGAGGGCGCTGAGGCGTCCAGGCGCTGAGAGGCTGAGGCTGAGGCTGAGGCTT 1593
Db      1528  CAAGAGGGCGCTGAGGCGTCCAGGCGCTGAGAGGCTGAGGCTGAGGCTGAGGCTT 1586
Qy      1594  GAGCCCTGTCCCTGCGGCTGT 1614

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Db 1365 TGAAGC 1371

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RESULT 8  
US-09-417-197-138  
; Sequence 138; Application US/09417197  
; Patent No. 6518021  
; GENERAL INFORMATION:  
; APPLICANT: Ole Thastrup, et al.  
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An  
; FILE REFERENCE: 3759-0110P  
; CURRENT APPLICATION NUMBER: US/09/417,197  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 138  
; LENGTH: 2184  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE: EGFP-PKB fusion  
; NAME/KEY: CDS  
; LOCATION: (1)..(2181)  
US-09-417-197-138

Query Match 14.4%; Score 260.8; DB 4; Length 2184;  
Best Local Similarity 57.0%; Pred. No. 1e-51;  
Matches 517; Conservative 0; Mismatches 384; Indels 6; Gaps 2;

QY 343 GGGCTATGCGAAGGTTTCCAGGTGCGAAGGCGCAAGGCAACCACTTGGGCAAAATATA 402  
Db 1209 GGGCAAGGCGCTTCCGCAAGGATGATCTGTGTAAGAGAGCCACAGGCGCTACTA 1268  
QY 403 TGCATGAAAGTCTTAAGAAAGCCAAATGTGCGCAATGCCAAGACAAGACACAC 462  
Db 1269 CGCATGAAAGTCTTCAAGAAAGATCATGTGCGCAAGAGG---TGGCCACAC 1325  
QY 463 ACGGCTGAGCGGAACTTTAGATGAGTGAAGCAACCCCTTATTTGTAATGGCGTA 522  
Db 1326 ACTGACCGAAGACCGGCTCTGCAAGATCTCAGGACCCCTTCTCAACACCTTGAAGTA 1385  
QY 523 TGCCTTCAGACTGTGCGCAAACTCTACTCTTGTGATGCTCAGTGTGCGAGCT 582  
Db 1386 CTCTTTCAGACCCAGACCGGCTCTGCTTGTGATGAGTAAGCCAAAGGCGGCGAGCT 1445  
QY 583 CTTCAGCATCTGAGCGAAGAGGCGCATCTTCTGAAAGATAGCGCTGCTTTACTGCG 642  
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QY 643 TGAATCAGCTGCGCTTGGGCGCATCTCACTC---CAAGGCAATCATACCGGAGCT 699  
Db 1506 TGAATGTGTCAAGCTTGAATCTGACCTGAGAGAGAAAGTGTGTATACCGGAGCT 1565  
QY 700 CAAGCCGAGAACTATCTGTCAGACGACGAGGCGCATCAATCAACTGACCGACTTTGACT 759  
Db 1566 CAAGCTGAGAACTCTGTCAGCAAGAGCGGCGCATTAAGATCAAGACTTCCGAGCT 1625  
QY 760 CTGCAAGAGTCTTATCCATGAGGCGCGCTCATCTCACTCTGCGGCGCACTTGAAGTA 819  
Db 1626 GTTCAGAGAGAGGATCAAGAGCGGTGCACTGAGAGAACTTTTGGGCGCACTTGAAGTA 1685  
QY 820 CATGCGCTTGAATTTCTGTGCGCAGTGGCAAAACCGGCGTGTGAGTGTGAGCGCT 879  
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Db 1746 GGGGCGGTATATGAGCAATGAGTGTGCGCTGCGCTTTTACCAACGAGAGCAATGA 1805  
QY 940 GAAACCATGATATGATCATCAGGCGCAAGTGGCACTGCGCGCTTACTCAACCCAGA 999

Db 1806 GAAGCTTTTGAAGCTATCTCTGAGAGAGATCCCTTCCCGGCAAGCTTGGTCCGA 1865

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RESULT 9  
US-09-212-771-1  
; Sequence 1; Application US/09212771  
; Patent No. 5958773  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Lex M. Cowsett  
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION  
; FILE REFERENCE: RTS-0034  
; CURRENT APPLICATION NUMBER: US/09/212,771  
; NUMBER OF SEQ ID NOS: 47  
; LENGTH: 2610  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE: CDS  
; NAME/KEY: CDS  
; LOCATION: (199)..(1641)  
US-09-212-771-1

Query Match 14.4%; Score 260.8; DB 2; Length 2610;  
Best Local Similarity 57.0%; Pred. No. 1e-51;  
Matches 517; Conservative 0; Mismatches 384; Indels 6; Gaps 2;

QY 343 GGGCTATGCGAAGTGTTCAGGTGCGAAGGCGCAAGGCAACCACTTGGGCAAAATATA 402  
Db 666 GGGCAAGGCGCACTTTCGCAAGGTATCTGTGTAAGAGAGGCGCAAGGCGGCTACTA 725  
QY 403 TGCATGAAAGTCTTAAGAAAGCCAAATTTGTGCGCAATGCCAAGACAAGACACAC 462  
Db 726 GGCATGAAAGTCTTCAAGAAAGATCATGTGCGCAAGAGAGG---TGGCCACAC 782  
QY 463 ACGGCTGAGCGGAACTTCTAGTCACTGAGTGAAGACCCCTTATTTGTAAGTGTGAGCT 522  
Db 783 ACTCAACGAGAACCGGCTCTGCAAGATCTCAGGACCCCTTCTCAAGCGCTTGAAGTA 842  
QY 523 TGCCTTCAGACTGTGCGCAAACTCTACTATCTTGAAGTCTGAGTGTGAGCGAGCT 582  
Db 843 CTCTTTCAGACCCAGACCGGCTCTGCTTGTGTAAGAGTACGCGCAAGGCGGCGAGCT 902  
QY 583 CTTCAGCATCTGAGCGAAGAGGCGATCTTCTGTAAGATAGGCGCTGCTTACTGAGC 642  
Db 903 GTTCTTCACTGTGCTCCGGAAGCGTGTGTTCTCCAGAGACCGGCGCGCTTATAGGCGC 962  
QY 643 TGAATCAGCTGCGCTTGGGCGCATCTCACTC---CAAGGCAATCATCTACCGGAGCT 699  
Db 963 TGAATGTGTGAGCGCTGAGTCACTGAGAGAAAGTGTGTATACCGGAGCT 1022

Qy	700	CAAGCCCGGAACATCATCTCTCAGACGCGAGGGCCACATCAACATGACCGACTTGGAGCT	759
Dp	1023	CAAGCTGAGAACTCTATCTCTGAGACAAGGACGGGACATTAAGATCAAGACTTGGGCT	1082
Qy	760	CTGCACAGAGCTTATTCATGAGGGGGCCCTCACTCAACCTTCTGCGGCACATTAGTA	819
Dp	1083	GTGCACAGAGGGGGAATCAAGGACGGTCCACACATGAAGACTTTTCCGGCACACCTGAGTA	1142
Qy	820	CATGGCCCCCTGAGATCTGTGCGGAGTGGCCACAAACCGGGGCTGTGGAATGGAGCT	879
Dp	1143	CTTGCCCCCGAGGCTGCTGAGAGACATTAAGTACGGCCCTGTGAGTGTGTGGGAGCT	1202
-Qy	880	GGGGGCCCCGATGTATGACATGCTCACTGATGCGCGCCCTTTACCGCAGAAACCGGAA	939
Dp	1203	GGGGCGTGTGATGTACGAGATGATGTGGGTGTGCGCTGCCCTTTCTPACAAACGAGAACATGA	1266
Qy	940	GAHAACATGATTAAGATCATGAGGGGCAAGCTGGGACGTGCCCCCTTACTTCACCCACGA	999
Dp	1263	GAGCTTTTGTAGCTTATCTCATGTAGAGAGATGCGCTTCCGGCCACGCTTGTGTCGGA	1322
Qy	1000	TGCCCCGGACCTTGTCAAAAAGTTTCTGAAAAGAAATCCAGCCAGCGGATTTGGGGGTGG	1059
Dp	1323	GGCCAGATCTTGTCTTTAGGGCTGTCTAAGAGAACCCCAAGAGAGGCTTGGGGGGG	1382
Qy	1060	CCGAGGGGATGCTGCTGATGTGCAAGACATCCCTTTTCCGGCACATGAATTGGGACGA	1119
Dp	1383	CTCCAGGACGCGCAAGAGATCATGCAGATGCTTCTTGGCGGTATGTTGTGGCACCA	1442
Qy	1120	CTTTGTGCGCTGGCGTGTGGAACCCCTTTTCAGGCGCTGTGCAAGTACAGAGAGAGT	1179
Dp	1443	CGTGTACAGAAAGAAAGCTCAGCCGACCTTTCAAGCCCAAGGTCAAGTGTGAGACTGACAC	1502
Qy	1180	GAGCCAGTTGATATACCCGCTTCACACGCGCAGACGCGCGGTGACAGTCTCTGTACACAGC	1239
Dp	1503	CAGGTATTTTGTATGAGAGTTTCAAGGCCCAAGTATGACATTCACACCACTGACCAAGA	1562
Qy	1240	CCTCAGC 1246	
Dp	1563	TGACAGC 1569	
RESULT 10			
US-09-091-058-1			
Sequence 1, Application US/09091058			
Patent No. 6054285			
GENERAL INFORMATION:			
APPLICANT: Hemmings, Brian A.			
APPLICANT: Frech, Mathias			
TITLE OF INVENTION: Screening Method			
FILE REFERENCE: 4-20683/A/20184/PCT			
CURRENT APPLICATION NUMBER: US/09/091.058			
CURRENT FILING DATE: 1998-06-10			
EARLIER APPLICATION NUMBER: PCT/EP96/04814			
EARLIER FILING DATE: 1996-11-05			
EARLIER APPLICATION NUMBER: 9525703.6			
EARLIER FILING DATE: 1995-12-15			
NUMBER OF SEQ ID NOS: 23			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO 1			
LENGTH: 2610			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (199)..(1641)			
US-09-091-058-1			

Query Match	14.4%	Score 250.8	DB 3	length 2610
Best Local Similarity	57.0%	Pred. No. 11e-51		
Matches 517	Conservative	84	Indels	6
			Gaps	2
QY	343	GAGCATATGACAAAGGTCTTCAGAGTCCGAAAGGTGCAAGGCAACCACTTGGGCAAAATATA	402	

Db	666	GGGCAAGGACACTTTTGGCAAGGTGATGCTGTGTGAAGAGAAAGGCCACAGGCGCTACTA	725
Qy	403	TGCCATGAAAGTCTTAAGAAAGGCCAAATATGTGCGCAATGCCAAAGACACAGCACAC	462
Db	726	CCCCATGAAAGTCTTAAGAAAGGAGTATGATGATGCGCAAGACGAGG---TGGCCCAAC	782
Qy	463	ACGGGCTAGCGGAACATTCTTAGAGTCAGTGAAGACACCCCTTATTTGTGAACCTGGACCTA	522
Db	783	ACTCACCGAAGAACCGCGTCTCTGCAAACTCCAGGACACCCCTTCTCAACGCCCTGAAATA	842
Qy	523	TGCTTCCAGACTGGTGGCAAACTTCACTCACTTGAAGTCCAGTGGTGGAGCT	582
Db	843	CTCTTCCAGACCCACGACCCCGCTCTGCTTTGTCAATGAGATACGCCAACGGGGGGGAACT	902
Qy	583	CTTCAOGATCTTGAGAGCGAGGGGCACTTCTGTGAAGATACGGCTGCTTCACTGAC	642
Db	903	GTTCTTCAACTGTCCCGGGAACGTGATTTCTCCAGGACCGGGCGCCCTTCTATGGCGC	962
Qy	643	TGAGATCAAGCTGGCGCTGGGCCATCTTCCACTC---CCAGGGCATTCATCTACCGGACCT	699
Db	963	TGAGATTTGTGACGCCCTTGACTACCTGCACTCCGAGAAAGAACGTGGTGTACCGGACCT	1022
Qy	700	CAAGGCCCAAACTATATGCTTCAACGCGAAGGCGCAATCAAACTGACCGCACTTGGACT	759
Db	1023	CAAGTGTAGAACCTCATGCTTGACAAAGAGAGGGGCACTTAAGATCAACAGACTTGGGCT	1082
Qy	760	CTGCAGAGATCTATCCATGAGGGCGCGCTCACTCAACCTTCTGCGGCAACATTGAGTA	819
Db	1083	GTGCAGAGAGGGGATCAAGAGAGGTGCACATGAAGACTTTTGGCGCAACCTGAGTA	1142
Qy	820	CATGGCCCTTGAATTTCTGTGGCGCAGTGGCCACAACTGGGCTGTGAATGTGTGAGCT	879
Db	1143	CCTGGCCCCAGAGGTGTGAGAGCAATGACTAGCGCGTGCAGTGTGACTGTGTGGGCT	1202
Qy	880	GAGGGGCCCTGATGTACGACATGCTCACTGATGCGCGCGCTTTTACCGCAGAAACCGGAA	939
Db	1203	GGGGTGTGATGTATGAGATGATGTGCGGTGCGCTGCTCTTCAACACGAGACATGA	1262
Qy	940	GAAAAACATGATTAAGATCATCAGGGGCAAGCTGGCACTGCCCTCTACTCACTCCAGA	999
Db	1263	GAACTTTTGAAGCTCACTCCATCAGAGAGAGATCCGCTCCCGGCAACGCTGTCCCA	1322
Qy	1000	TGCCCGGACCTTGTCAAAAAGTTCTGAAAOGGAATCCAGCGCAGGGATTTGGGGGTGG	1059
Db	1323	GGCCAAGCTCTGCTTTCAAGGCTGCTCGAAGAAAGACCCCAAGCAAGGCTTGGCGGGG	1382
Qy	1060	CCAGAGGATGCTCTGATGTGCAGAGACATCCCTTTTTCGGGCACTGAATTGGACGA	1119
Db	1383	CTCCGAGAGCGCCAAAGGATCATGAGCAATGGCTTCTTGGCGGTATGATGTGGACGA	1442
Qy	1120	CCTTCTGGCGCTGGGTGTGAACCCCTTTCAAGGCTGTGTGTGCAATCAGAGAGAGAGT	1179
Db	1443	CGTGTACGAGAAAGGCTCAGGCCACCTTTCAAGCCGCCAGGTCACTGTGAGACTGAC	1502
Qy	1180	GAGCCAGTTGATATCCCGTTTCAACCGGCAAGCGCGGTGACAGTCTGTGACAGACG	1239
Db	1503	CAGGTATTTGATGATGAGAGGTTCAAGCGGCCAGATGATCAACATCAACACCTGACAA	1562
Qy	1240	CCTCAGC 1246	
Db	1563	TGACAGC 1569	

```

RESULT 11
US-09-023-655-1206
; Sequence 1206, Application US/09023655
; Patent No. 6607879
;
; GENERAL INFORMATION:
;
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Sellhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENES
; TITLE OF INVENTION: EXPRESSION

```

NUMBER OF SEQUENCES: 1508  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 STREET: 3174 PORTER DRIVE  
 CITY: PALO ALTO  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/023,655  
 FILING DATE: HEREMITH  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Zeller, Karen J.  
 REGISTRATION NUMBER: 37,071  
 REFERENCE/DOCKET NUMBER: PA-0001 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 855-0555  
 TELEFAX: (650) 845-4166  
 INFORMATION FOR SEQ ID NO: 1206:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2610 base pairs  
 TYPE: nucleic acid  
 STRANDBESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GENBANK  
 CLONE: g190827  
 US-09-023-655-1206

Query Match 14.4%; Score 260.8; DB 4; Length 2610;  
 Best Local Similarity 57.0%; Pred. No. 1,1e-51;  
 Matches 517; Conservative 0; Mismatches 384; Indels 6; Gaps 2;

QY 343 GGGCTATGCGAAGGTGTTCCAGGTGCGAAGAGTGCAGCAACCACTTGGGCAAAATATA 402  
 DB 666 GGGCAAGGCACTTCGGCAAGGTGATCTGTGAGAGAGAGGCAAGCCGCTACTA 725  
 QY 403 TGCCATGAAGTCTTAAGAGAGGCAAAATTTGGCGAATGCCAAGCAACAGACAC 462  
 DB 726 CGCATGAAGATCTCAAGAGAGAGTCACTGTGGCCAGAGAGAGG--TGCCCAAC 782  
 QY 463 ACGGGCTGAAGCGGAACTTGAAGTCAAGAGCAACCCCTTATTTGTGAACTGGCTA 522  
 DB 783 ACTCAACGAGAACCGGCTCTGAGAACTCAGAGCAACCCCTTCTCAACCCCTGAAGTA 842  
 QY 523 TGCCCTTCAGACGTGTGGCAAACTTACCTCACTCTTGAATGCTCAATGTGGCGAGCT 582  
 DB 843 CTCTTTCAGACCCAGCAACCGCTCTGTCTTGTGATGAGATAGCCAAACGCGGCGAGCT 902  
 QY 583 CTTCAGCATCTGAGAGAGAGGAGCATCTTCTGAGAGATACGGCTGTCTTACTTGGC 642  
 DB 903 GTTCTTCACTCTGCGGAGAGAGTGTCTCCGAGAGACGGGCGCGCTTCTAAGGCGC 962  
 QY 643 TGAATACAGCTGCGCTGGGCAATCTCACTC---CGAGGCACTATCTACCGGAGCT 699  
 DB 963 TGAATGTGTGACCGCTGAGTACTGCACTCGAGAGAGAGAGTGTATCGGAGACT 1022  
 QY 700 CAAGCCGAGAGACATCATGCTCAGACAGCGGCGCAATCAACGATCTTGAAGT 759  
 DB 1023 CAAGCTGAGAGACCTCATGCTGAGACAGAGAGGCGACATTAAGATCAAGACTTGGGCT 1082  
 QY 760 CTGCAAGAGCTTATTCAGAGAGGCGCTCACTCAACCTTCTGCGGCAACATTAAGTA 819

DB 1083 GTGCAAGAGAGGATCAAGACGCTGCCACATGAAGACCTTTTGGCGACACTGAGTA 1142  
 QY 820 CATGCCCCCTGAGATTCTGTGCGCACTGAGCCACACCGGCTGTGATCTGTGAGAGCT 879  
 DB 1143 CTTGCCCCCGAGGTCTGAGAGGACATGACTAGCCGCTGTGAGTGTGTGGGGCT 1202  
 QY 880 GGGGCGCTGATGATGAGACATGCTCACTGATGCGCGCCCTTTACCGGAGAGAACGGGA 939  
 DB 1203 GGGCGTGTATGATGAGAGATGATGTGCGGTGCGTCCCTTTCAACACGAGACATGA 1262  
 QY 940 GAAACCATGATATGATCATCAAGGGCAAGTGGCACTGCGCCCTTACCTCAACCCGAGA 999  
 DB 1263 GAAGCTTTTGAAGTCACTCTTCAAGAGAGATCCGCTTCCGCGACGCTGTCCCGA 1322  
 QY 1000 TGCCCGGAGCTTGTCAAAAGTTTCTGAACGAGATCCAGCCAGATTGGGGGTG 1059  
 DB 1323 GGGCAAGTCTTCTTCAAGGGCTGTCAAGAGAGACCCAGAGCAGAGCTTGGCGGAG 1382  
 QY 1060 CCCAGGGAGTGTGATGATGTCAGAGACATCCCTTTTCGCGCAGATGAATTGGAGCA 1119  
 DB 1383 CTCCGAGAGCCAGAGAGATCATGACAGCTGCTTCTTGGCGATTCGTGTGGCAGCA 1442  
 QY 1120 CTTTGGCGCTGCGGTGTGACCCCTTTCAGGCTCTGTCTGACATGACAGAGAGAGT 1179  
 DB 1443 CGTGTACGAGAGAGAGCTCAGCCCACTTCAAGCCCAAGTACAGCTGAGACTGAC 1502  
 QY 1180 GAGCCAGTTGATATCCCGCTTCAAGGACAGAGCGCGGTGAGATCTGATGACAGC 1239  
 DB 1503 CAGGTATTTTGAAGAGAGTTCAGGCGCCAGATGATCAACATCAACCACTGACAA 1562  
 QY 1240 CCTCAGC 1246  
 DB 1563 TGAACAGC 1569

RESULT 12  
 US-09-256-465-1  
 ; Sequence 1, Application US/09256465  
 ; Patent No. 6043090  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Brett P. Monia  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION  
 ; FILE REFERENCE: RTS-0035  
 ; CURRENT APPLICATION NUMBER: US/09/256,465  
 ; CURRENT FILING DATE: 1999-02-23  
 ; NUMBER OF SEQ ID NOS: 47  
 ; SEQ ID NO 1  
 ; LENGTH: 1599  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (88)..(1533)  
 US-09-256-465-1

Query Match 14.0%; Score 253.8; DB 3; Length 1599;  
 Best Local Similarity 54.0%; Pred. No. 4,1e-50;  
 Matches 569; Conservative 0; Mismatches 472; Indels 12; Gaps 2;

QY 313 CTTTGAAGCTGCGGTGTGTCGAGAGGGGCTATGCGCAAGGTGTCAGGTGCGAAA 372  
 DB 540 CTTTGAAGCTGCGGTGTGTCGAGAGGGGCTATGCGCAAGGTGTCAGGTGCGAAA 599  
 QY 373 GGTGCAAGGCAACCTTGGGCAAAATATATGCGATGAAGTCTTAAGAGAGGCCAAAT 432  
 DB 600 G-----AAGGCACTGGCGCTTACTAGCGCATGAAGATCTGCGAAGAGAGTAT 650  
 QY 433 TGTGCGCAATGCGCAAGACAGACAGACAGCGGCTTGAAGGCAATCTTGAAGTCACT 492  
 DB 651 CATTCGCAAGG---ATGAAGTGTCTCAACAGTCAACGAGAGCGGCTCTTCAAGAAC 707  
 QY 493 GAAGCAACCCCTTATTTGTGAACTGCGCTATGCTTTCAGACTGTGCGCAACTTACT 552

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Db 708 CAGGCAACCCCTTCTCTACGCGCTGAGATATGCTTCCAGACCCAGACCCGCTTGTCTT 767
Qy 553 CATCTTGAAGTCCCTCAAGTGTGGCGAGCTTTTCAAGCATTTGAGCGAGAGGCAATCTT 612
Db 768 TGTGATGAGATATGCGCAAGCGGGGTGAGCTGTTCTTCCACTGTCTCCGGAGAGGTGTCTT 827
Qy 613 CCGGAGAGATACGGGCTGCTTCTTACCTGCGAGATACAGCTGCGCTGGGCCATCTCCA 672
Db 828 CACAGAGAGAGGAGCGCGGCTTTTATGCTGAGAGATTTCTCGCTCTTGAATCTTGA 867
Qy 673 CTCCAGAGGAGCATATCTACCGGAGCCTCAAGCCCGAGAGACATATGCTCAGACCGAGG 732
Db 888 CTGCGGAGAGCTGTATACCGGAGCATCAAGCTGAGAAAACCTCATGCTGGACAAAGATGG 947
Qy 733 CCACATAAACTAGACCGACTTGGACCTGCGAGAGAGTCTATCCATCAAGGCGCGCTCAC 792
Db 948 CCACATAGATCATCTGACTTGTGCTTGGCAAGAGGAGCATGATGACGGGCGCACAT 1007
Qy 793 TCACACTTCTGCGGAGCATATGAGTACATAGCGCCCTGAGATTCTGGTGGCAGTGGCA 852
Db 1008 GAAACCTTCTGTGGAGCCCGGAGTACCTGGCGCTGAGGTCTGGAGGACATGACTA 1067
Qy 853 CAACCGGAGCTGTGAGCTGTGAGAGCTGGGGGCTGATGTATGACATGCTCACTGGATC 912
Db 1068 TGGCGGAGCGTGTGAGCTGTGGGGGCTGGGTGTGATGATGAGATGATGTGGCGCG 1127
Qy 913 GCGGCTTCTTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 972
Db 1128 CTGCGCTTCTTAAACAGAGACCAAGAGCGCTCTTGAAGTCTCTGATGAGAGAGAT 1187
Qy 973 GAGACTGCGCCCTTACTCTCAACCCAGATGCGCGGAGCCTTGTCAAAAAGTTTCTGAACG 1032
Db 1188 CCGCTTCTCGGAGAGCTCAAGCCCGAGGCGAGTCTCTGCTGGCTGCTTAAAGAA 1247
Qy 1033 GAATCCAGCGAGAGATTTGGGGGTGGGCCCGAGGAGTGTGCTGATGTGAGAGAGATCC 1092
Db 1248 GAGCCCGAGAGAGAGCTTGTGGGGGCGCCAGAGAGTGTGAGAGAGTCTGAGAGAGAG 1307
Qy 1093 CTTTTCGCGAGCATGATTTGAGAGAGCCTTCTGGCGCTGGCGCTGTGAGAGAGAGAG 1152
Db 1308 GTTCTTCTGAGCATCACTGCGAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG 1367
Qy 1153 GCGCTTCTGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1212
Db 1368 ACTCAAGTCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1427
Qy 1213 GCGGAGAGAGAGTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1272
Db 1428 CATCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1487
Qy 1273 CTTCAATAGTGTGGCGCGCTGTCTGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1332
Db 1488 GAGCCAGTCTTCCCGAGTCTCTCACTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1547
Qy 1333 CAAGCTGCGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1365
Db 1548 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1580

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RESULT 13  
 US-09-167-322-3  
 Sequence 3, Application US/09167322  
 Patent No. 6365151

## GENERAL INFORMATION:

APPLICANT: Allegheny University of the Health  
 Sciences, Halpern, Michael S.  
 England, James M.  
 TITLE OF INVENTION: CANCER VACCINE  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Seidel, Conda, Lavoigna & Monaco, P.C.  
 STREET: Suite 1800, Two Penn Center Plaza

```

? CITY: Philadelphia
? STATE: PA
? COUNTRY: USA
? ZIP: 19102
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/167,322
? FILING DATE: 07-Oct-1998
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/US97/00582
? FILING DATE: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Monaco, Daniel A.
? REGISTRATION NUMBER: 30,480
? REFERENCE/DOCKET NUMBER: 7933-33 PC
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (215) 568-8383
? TELEFAX: (215) 568-5549
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1599 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? SEQUENCE DESCRIPTION: SEQ ID NO: 3:
?
? US-09-167-322-3
?
? Query Match 14.0%; Score 253.8; DB 4; Length 1599;
? Best Local Similarity 54.0%; Pred. No. 4.1e-50;
? Matches 569; Conservative 0; Mismatches 472; Indels 12; Gaps 2;

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## Alignment Scores:

Pred. No.: 6,27e-159 Length: 1637  
 Score: 1947.50 Matches: 407  
 Percent Similarity: 90.89% Conservative: 2  
 Best Local Similarity: 90.44% Mismatches: 34  
 Query Match: 74.50% Indels: 13  
 DB: 2 Gaps: 4

US-09-762-258-2 (1-495) x US-08-966-316-10 (1-1637)

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QY 9 G1YAlaG1YAlaAlaMeValAlaValPheAspLeuSerLeuGluThrGluGluGlySer 28
Db 180 GGGGGCCGCGCCGCGCATGCGCGCGTGTGATTGATTGATTGAGAGCGAGAGAGCGAGC 239
QY 29 G1uG1yG1uG1yG1uPProG1uLeuSerProAlaAspAlaCysProLeuAlaGluLeuArg 48
Db 240 GAGGGCGAGGGCGAGCGAGCGAGCTCAGCCCGGAGCGCAGTCCCTTGCGAGTTGAGG 299
QY 49 AlaAlaG1yLeuGluPProValG1YH1sTyG1uG1uValG1uLeuThrG1uThrSerVal 68
Db 300 GCGCTGCGCTAGAGCGCTGTGGACACTATGAGAAGGTGGAGCTGACTGAGAGCCAGCTG 359
QY 69 AsnValG1yPProG1uArg1LeG1yProH1sCysPheGluLeuLeuArgValLeuGlyLys 88
Db 360 AACGTGGCCCGAGCGCGCATCGCGCCCGCATGCTTGAGCTGCTGTGCTGCGGCAAG 419
QY 89 G1yG1yTyG1yLysValPheG1uValArgPysValG1uG1yThrAsnLeuGlyLys1Le 108
Db 420 GGGGGCTATGGCAAGGTGTTCCAGGTGCGAAGGTGCGAAGCGACCACTTGCGCAATA 479
QY 109 TyrAlaMetLysValLeuArgLysAlaLys1LeValArgAsnAlaLysAspThrAlaHis 128
Db 480 TATCCCATGAAGTCTTAAGAGAGCGCAAAATGTGTGGCATGTGCAAGACAGACAGCAC 539
QY 129 ThrArgAlaG1uArgAsn1LeuGluSerValLysHisProPhe1LeValG1uLeuAla 148
Db 540 ACAGGGCTAGCGCGAAGCATTTCTAGAGTGAAGAGACCCCTTATGTGGAAGCTGGCC 599
QY 149 TyrAlaPheG1uThrG1yG1yLysLeuTyrLeu1LeuG1uCysLeuSerG1yG1yG1 168
Db 600 TATCCCTTCCAGATGTGTGGCAACTTACTTACTTCTTGATTGCTCTGCTGTGGCGA 659
QY 168 uLeuPheThrHisLeuGluArgG1uG1y1LePheLeuGluAspThrAlaCysPheTyrLe 188
Db 660 GCTCTTCAAGCATCTGAGCGAGCGAGCGCATCTTCTGAGAGATCGCGCTGCTTCTACT 719
QY 188 uAlaG1u1LeuThrLeuAlaLeuG1yH1sLeuHisSerG1uG1y1Le1LeTyrArgAspLe 208
Db 720 GAGTGAATCAAGCTGGCGCTGGCGCTGCTCACTCTCCAGGCGCATCTACCGGAGACT 779
QY 208 uLysPProG1uAsn1LeuMetLeuSerSerG1uG1yH1s1LeLysLeuThrAspPheGlyLe 228
Db 780 CAAAGCCGAGAGCAATCAATGCTCAGACAGCGCGCAATCAAACTGACCGACCTTGAGCT 839
QY 228 uCysLeuG1uSer1LeHisG1uG1yAlaValThrHisThrPheCysG1yThr1LeG1y 248
Db 840 CTGCAAGAGTCTATCAATGAGGGCGCGTCACTCAACACCTTCTGCGCGACCATATGAGTA 899
QY 248 rMetAlaPProG1u1LeuValArgSerG1yH1sAsnArgAlaValAspTyrTrpSerLe 268
Db 900 CATGGCCCTGAGATTCTGGTGGCGAGTGGCCAAACCGGGCTGTGAGCTGTGGAGACT 959
QY 268 uG1yAlaLeuMetLysAspMetLeuThrG1ySerProProPheThrAlaGluAsnArgLys 288
Db 960 GGGGGCCCTGATGATACACATGCTCACTGAGATCCCGCTTCAACCGAGAGAACCGGAA 1019
QY 288 sLysThrMetAspLys1Le1LeArgG1yLysLeuAlaLeuProProTyrLeuThrProAs 308
Db 1020 GAAAGACATGATTAAGATCATCAGGGGCGAGCTGCGCCCTTCACTCACTCAACCGACA 1079
QY 308 pAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerG1uArg1LeG1yG1y 328
  
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Db 1080 TGCCCGGAGACTTGTCAAAAAGTTTCTGAACCGAATCCAGCCAGCGGATGGGGGTGG 1139
QY 328 YProG1yAspAlaAlaAspValG1uArgHisProPheArgHisMetAsnTrpAspAs 348
Db 1140 CCCAGGGAGAGCTGCTGATGTGAGAGACATCCCTTTTCCGGCACATGAATGGAGCGA 1199
QY 348 pLeuLeuAlaTrpArgValAspProProPheArgProCysLeuG1uSerG1uG1uAspV 368
Db 1200 CTTCTGGCTGGCGGTGTGAGAACCCCTTTCAAGGCCCTTCTGTCACTCAGAGAGAGCT 1258
QY 368 aLseG1uPheAspThrArgPheThrArgG1uThrProValAspSerProAspAspThrA 388
Db 1259 --GAGAGTTTGAATACCCGCTTCAACCGGACAGCGCGGTGACAGTCTGATGACAG 1316
QY 388 lLeuSerG1uSerAlaAsnG1uAlaPheLeuG1yPheThrTyrValAlaProSerVal 408
Db 1317 C-CTCAGCGAGAGTGTCAACAGGCTTCTGCGGTT-ACATAGTGGCGCG-TCGTCC 1373
QY 408 euAspSer1LeuG1yG1yPheSerPheG1uProLysLeuArgSerProArgArgLeuA 428
Db 1374 TGAGCAG-ATCAGAGAGS---TTCTTTTACGCCAAGT-----GGGTCAACAGGCTC 1423
QY 428 snSerSerProArgValProValSerProLeuLysPheSerProPheG1uG1yPheArgP 448
Db 1424 AANATAGCCCGCGG--TCCGTAGGCC--TCAAGTTTCCCTTMAAGGTTCCGCCA 1477
QY 448 roSerProSerLeuPProG1uProThr 466
Db 1478 GCCACCTTMCNGGCCAAGAGTACT 1503
  
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## RESULT 3

US-09-817-310-1

; Sequence 1, Application US/09817310

; Patent No. 6534311

; GENERAL INFORMATION:

; APPLICANT: Stewart, Mary

; APPLICANT: Kozma, Sarah

; APPLICANT: Thomas, George

; TITLE OF INVENTION: Drosophila melanogaster P70 S6 Kinase

; FILE REFERENCE: 4-20971/A

; CURRENT APPLICATION NUMBER: US/09/817,310

; PRIORITY FILING DATE: 2001-03-26

; PRIORITY FILING DATE: 1999-04-16

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 2556

; TYPE: DNA

; ORGANISM: Drosophila melanogaster

US-09-817-310-1

## Alignment Scores:

Pred. No.: 4.3e-116 Length: 2556  
 Score: 1455.00 Matches: 309  
 Percent Similarity: 66.73% Conservative: 52  
 Best Local Similarity: 57.12% Mismatches: 115  
 Query Match: 55.66% Indels: 65  
 DB: 4 Gaps: 10

US-09-762-258-2 (1-495) x US-09-817-310-1 (1-2556)

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QY 13 AlaMetAlaAlaVal-----PheAspLeu-----AspLeuGlu 23
Db 471 GCATGCGGAGCGTGAAGCATCCAGCGAGACTGTTGACCTGGAGCTGCAGACCTGGAA 530
QY 24 ThrGluGluG1ySerG1uG1yG1uG1uPro-----GluLeuSerProAlaAsp 40
Db 531 CTGCAAGAGAGCAAGCGCGAGGACTCCAGAGAGAGATGAGAGTGAAGCGAGCTTGAC 590
QY 41 AlaCysProLeuAlaGluLeuArgAlaAlaG1yLeuGluProValG1yH1sTyG1uG1u 60
Db 591 CTAGAACCG-----GAATTGTGATTAATCTGACCAAGACACTGAGGCGCAGAGAAC 644
  
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QY	61	ValGluLeuThrGluThrSerValAsnValGlyProGluAspIleGlyProHisLeuSerPhe	80
Db	645	ATACAGCTCTCGCAGAGAGATTTATCCAGGTAAATACAGCTGGACCCAGACATTT	704
QY	81	GluLeuLeuArgValIleuGlyLysGlyGlyTyrGlyLysValPheGlnValArgLysVal	100
Db	705	GAGCTCAAGAAAGTCTCTGGCAAGCGGTATTCGCAAAAGTATTTACAGGTGGCAAGCC	764
QY	101	GlnGlyThrAsnLeuGlyLysIleTyrAlaMetLysValIleuArgLysAlaLysIleVal	120
Db	765	GCTGACACGAGATGCTAACCAATTTTGGCATGAAGTCTCAAAAAGCATCCATTGTG	824
QY	121	ArgAsnAlaLysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLys	140
Db	825	ACCATCAAAAGACACAGCCGACACCCGCGCCGACCAATATCTCGAGGCACATCTCAG	884
QY	141	HisProPheIleValGluLeuAlaTyrAlaPheGlnTrnGlyLysLysLeuTyrLeuIle	160
Db	885	CATCCCTTCATAGTGGAGCTAGTTTATGCTCTCCAGACAGACGAAACCTATACCTTATA	944
QY	161	LeuGluCysLeuSerGlyGlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeu	180
Db	945	CTTGAAATATCTCAGCGGTGGAGAGCTGTTCATGCAATTTGGAGCGCGACATCTCTTA	1004
QY	181	GluAspThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisIleuHisSer	200
Db	1005	GAGATACACACATGCTTCTATCTAAGCAATTTTGCGCTTGGCCCATCTACACAA	1064
QY	201	GlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHis	220
Db	1065	CTGGGCATCATCTACCGGAGTCTGAAGCCCGAACAATCTGCTGAGACACAGGACAT	1124
QY	221	IleLysLeuTrnAspPheGlyLeuCysLysGluSerIleHisGluGlyValAlaValThrHis	240
Db	1125	GTAAGCTCAACGACCTTGACGTGGACGTGGACAGACACATACAAAGAGATTGTCAACCA	1184
QY	241	ThrPheCysGlyThrIleGlnTyrMetAlaProGluIleLeuValArgSerGlyHisAsn	260
Db	1185	ACCTTCTCGGACACAAATTGAGTACATGACACTGTAAATTTGACACAGAGTGGCCATGCG	1244
QY	261	ArgAlaValAspTrpTrpSerIleuGlyValAlaLeuMetTyrAspMetLeuThrGlySerPro	280
Db	1245	AAAGCAGTCGACTGATGTCTACTGGCCCTCTCACTTTGACATCTCAGAGATGCCA	1304
QY	281	ProPheThrAlaGluAsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAla	300
Db	1305	CCCTTCAACCGCGCAATGCGAAGAGACATCGAGACATCTGTAAAGCCAAAGCTCAAT	1364
QY	301	LeuProPheTyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsn	320
Db	1365	CTGCCAGCCTACCTCAACACCGAAGCCAGGATCTCGTGGCGCTGATGAAGCGGAG	1424
QY	321	ProSerGlnArgIleGlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhe	340
Db	1425	GAACCTCAGCCCTTGGCGAGCGGACCCGAGATGCGGCGCTGTCAAAATACACCCATTTC	1484
QY	341	PheArgHisMetLeuTrpAspAspLeuLeuAlaTrpArgValAspProProPheArgPro	360
Db	1485	TTCAACAACGTCACCTGGAGCGATGTCTCCGCCAACCCTCGAGCCGCTATATAAACCG	1544
QY	361	CysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPheThrArgGlnTrnPro	380
Db	1545	CTCTTGAAACACGAGATGATGTCTCAACAGTTCCATTAACAAATTCACAAAGCAATTC	1604
QY	381	ValAspSerProAspAspThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPhe	400
Db	1605	GTGATTTCCCTGATGATACAAACGCTAAGCGAAAGTGCACAAATTATTTCCAAAGTTTC	1664
QY	401	ThrTyrValAlaProSerValLeuAspSerIleLysGluGlyPheSerPheGlnProLys	420
Db	1665	ACCTACGTTGACCTCGATCTGAATCTGAAGATTAAGTACGCG-----GCCAACCGAGTCC	1718

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QY      421 LeuAnsSerProAArg-LeuAnsSerProAArgValProvalSer----- 436
Db      1719 GCAGGCTCCACACACGACTCTCACGCCAGCTGCCAGACAGACACTTCGCTGCAGTTC 1778
QY      437 -----ProLeuLysPheSerProPheGluGlyPhe----- 446
Db      1779 CCATCGGCCAATGTGGGCGCCCAATGCGCTGTGGCCATGCACGGTCAATCGACGCAATC 1838
QY      447 -----ArgProSe 449
Db      1839 CCGGATGTTTGCACAGACGACGCCGCCGATCAGATGCAGACATTTGGCGCGCTTCATC 1898
QY      449 rProSerLeuProGluProThrGlu-----LeuPro-----LeuProPr 462
Db      1899 GCCGCGCCAGGACGAGATGATGCAGCGTCTGCCAATGCTCTAAAGCTGGAGCG 1958
QY      462 oLeuLeuProProProProSerThrThrAlaProLeuProIleArgPro----- 479
Db      1959 ATTGCTTCCACACCAACCAACCAATCCCATCCGCTCGTTCGTCCGACACCAACAAGCTG 2018
QY      480 -----ProSerGlyThrLysLysSerLysArgGlyArg 492
Db      2019 CATCATAGCTTCTCTCTCTACCCCAAAAAAAAAAAAAAAAAAAAAAAG 2078
QY      492 G 492
Db      2079 A 2079

RESULT 4
US-08-749-902-4
; Sequence 4, Application US/08749902
; Patent No. 5985635
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
; TITLE OF INVENTION: PROTEIN KINASES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,902
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0150 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE:
; IS-08-749-902-4

```

## Alignment Scores:

Pred. No.: 2,21e-110 Length: 1607  
 Score: 1385.50 Matches: 285  
 Percent Similarity: 70.65% Conservative: 40  
 Best Local Similarity: 61.96% Mismatches: 69  
 Query Match: 53.00% Gaps: 67  
 DB: 2 Indels: 10

US-09-762-258-2 (1-495) x US-08-749-902-4 (1-1607)

QY 86 LeuGlyysGlyGlyTyrGlyLysValPheGlnValArgLysValGlnGlyThrAspLeu 105  
 DB 227 CTGGGGGAGGGCGCTCATGCCAGTGCAGACCTGC-----ATTAACTG 271  
 QY 106 -----GlyLysLeuTyrAlaMetLysValLeuArg-----LysAla 117  
 DB 272 ATCCACGACGAGGAGTACCCGTCACAAATCATGNTTTTTCAGAGCCACATTCGAGAC 331  
 QY 118 LysLeuValArgAsnAlaLysAspThrAlaHisThrArgAlaGluArgAsnLeuGlu 137  
 DB 332 AGCGTTTTCAGGAGAGTGGAGATGCTGTACCAAGTGCAGAGACACAGAAAGTCTTACAG 391  
 QY 138 SerVallyyHisProPheLleValGluLeuAlaTyrAlaPheGlnThrGlyLysLeu 157  
 DB 392 CTGATTAGTTC-----TTCCGAGGAGGAGACCGCTTC 424  
 QY 158 TyrLeuLeuGluGlyCysLeuSerGlyGlyLysLeuPheThrHisLeuGluArgGlu 177  
 DB 425 TACTGTGTTTGAAGAAGATCGGGAGAGCTCCATCTCCAGCCACATCCACAGAGCCCG 484  
 QY 178 IlePheLeuGluAspThrAlaCysPheTyrLeuAlaGluLeuThrLeuAlaLeuGlyHis 197  
 DB 485 CACTTCAACAGAGCTGAGAGCGAGCGTGTGTGAGAGAGCGGACCGCTTGGACTT 544  
 QY 198 LeuHisSerGlnGlyIleLeuTyrArgAspLeuLysProGluSerIleMetLeuSerSer 217  
 DB 545 CTGATACACAAAGGATCGCCCAAGGAGACCTAAAGCCGGAAGAAACATCTCTGTAGACAC 604  
 QY 218 GlnGlyHis-----IleLysLeuThrAspPheGlyLeu----- 228  
 DB 605 CCCAACAGAGTCTCCCGGAGATCTGTGACTGTGACCTGGGACGAGGATCAAACTC 664  
 QY 229 -----CysLysGlySerIleHisGluGlyAla-ValThrHisThrPheCysGlyThr 245  
 DB 665 AACGGGAGAGTCTCCCTCAT-CTCCACCCCGAGAGTCTCAGCTCCG-----TGGGCTC 717  
 QY 245 rIleGluTyrMetAlaProGluIle-----LeuValArgSerGlyHisAs 260  
 DB 718 GGGGAGTATCATGCCCCCGAGAGTATGAGAGGCTTCAGAGAGGATGCACTTACGA 777  
 QY 254 -----LeuValArgSerGlyHisAs 260  
 DB 778 CAAGCGCTGAGACCTGTGAGACCTGAGGCTCATCTGTATATCTACTCAGCGGCTACCC 837  
 QY 260 nArgAlaValAsp---ThrTrpSer-----LeuGlyAlaLeuMetTyrAspMetLe 276  
 DB 838 GCCCTTGTTGGCGCGCTGTGTGGAGCGCATGCGGCTGTGGACCGCTATATGACGACAGCT 897  
 QY 276 uThrGlySerProPheThrAlaGluAsnArgLysIleThrMetAspLysLeuLeu 296  
 DB 898 CACTGATGCGCGCGCTTATCCCGACAGAAACCGGAAACCATGATAGATATCATCG 957  
 QY 296 gGlyLysLeuAlaLeuProProGlyLeuThrProAspAlaArgAspLeuValLysLys 316  
 DB 958 GGGCAAGCTGCACTGCCCTTACCTCACCCAGATGCGCGGAGACCTTGTCAAAAAGTT 1017  
 QY 316 eleuLysArgAsnProSerGlnArgIleGlyGlyProGlyAspAlaAlaAspValG 336  
 DB 1018 TCTGAACGGAATCCACGCGAGGATGGGGGTGCGCCAGGGAGATGCTGATATGCA 1077  
 QY 336 nArgHisProPhePheArgHisMetAsnTrpAspAspLeuAlaTrpArgValAspPr 356

DB 1078 GAGCATCCCTTTTTCGGGACATGAATTGGAGAGACACTTCTGGCGCTGTGACCC 1137  
 QY 356 oProPheArgProCysLeuGlnSerGluAspValSerGlnPheAspThrArgPheTh 376  
 DB 1138 CCCCTTACGAGCCCTGTCTGTGAGTGCAGAGAGAGACGTGAGCCAGTTTATACCCCTTAC 1197  
 QY 376 rArgGlnThrProValAspSerProAspAspThrAlaLeuSerGlnSerLysAsnAl 396  
 DB 1198 AGCGACACCCCGGTGACAGTCTCTATGACACGCTCCAGAGAGATGCCACAGGC 1257  
 QY 396 aPheLeuGlyPheThrTyrValAlaProSerValLeuAspSerIleLysGlnGlyPhe 416  
 DB 1258 CTTCCTGGGCTTACATACAGCGCGCGCTGTGCTGTGAGACAGATCAAGAGAGGCTTCTC 1317  
 QY 416 rPheGlnProLysLeuArgSerProArgArgLeuAsnSerSerProArgValProVal 436  
 DB 1318 CTTCAGCCCAAGCTGCTGACCCAGGCGCTCAACAGAGGCCCGGGTCTCCCGTACG 1377  
 QY 436 rProLeuLysPheSerProPheGlnGlyPheArgProSerProSerLeuProGluPro 456  
 DB 1378 CCCCCTCAAGTTCTCCCTTTTGAAGGGTTTGGCCACAGCCACAGCTGCGGAGGCCAC 1437  
 QY 456 rGluLeuProLeuProProLeuLeuProProProProSerThrAlaProLeuPr 476  
 DB 1438 GAGACTAAGCTTCACTCTCACTCTGTCACCGCGCGCTCGACCAACCGCCCTCTCC 1497  
 QY 476 oIleArgProProSerGlyThrLysSerLysArgLysArgGlyArgProGlyArg 495  
 DB 1498 CATCTGTCCTCCCTCAGGACCAAGAGTCCAGAGGAGCGGTGGCGTCCAGGGCT 1555

RESULT 5  
 US-09-016-434-126  
 ; Sequence 126, Application US/09016434  
 ; Patent No. 6500938  
 GENERAL INFORMATION:  
 APPLICANT: Janice Au-Young  
 APPLICANT: Jeffrey J. Sellhammer  
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
 NUMBER OF SEQUENCES: 1490  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: INCYTE PHARMACEUTICALS, INC.  
 STREET: 3174 PORTER DRIVE  
 CITY: PALO ALTO  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/016.434  
 FILING DATE: HERewith  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Zeller, Karen J.  
 REGISTRATION NUMBER: 37,071  
 REFERENCE/DOCKET NUMBER: PA-0002 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 855-0555  
 TELEFAX: (650) 845-4166  
 INFORMATION FOR SEQ ID NO: 126:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1607 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

IMMEDIATE SOURCE:  
LIBRARY: COLPETO2  
CLONE: 1309709  
US-09-016-434-126

## Alignment Scores:

Pred. No.:	2,21e-110	Length:	1607
Score:	1385.50	Matches:	285
Percent Similarity:	70.65%	Conservative:	40
Best Local Similarity:	61.96%	Mismatches:	69
Query Match:	53.00%	Indels:	67
		Gaps:	10

US-09-762-258-2 (1-495) x US-09-016-434-126 (1-1607)

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QY 86 LeuGlyysgLygLygLygLygValPheGlnValArgLygValGlnGlyThrAspLeu 105
DB 227 CTGGGGAGGGCGCTCATGCGCCAGTGCAGACCTGC-----ATTAACTTG 271
QY 106 -----GlyysIeTyraIaMetLygValLeuArg-----LysAla 117
DB 272 ATCCAGCCAGGAGTACNCCGTCAANATCATTTTTCACAGCCACATTCGAGC 331
QY 118 LysIleValArgAsnAlaLysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGlu 137
DB 332 AGGGTTTCAGAGGAGTGCAGATGCTGTACCAAGTGCAGAGACACAGAGACGTCCTAGAG 391
QY 138 SerValysHisProPheIleValGluLeuAlaTyraIaPheGlnThrArgLygLygLeu 157
DB 392 CTGATGAGTTC-----TTCCAGAGGAGGACCGGCTTC 424
QY 158 TyrLeuIleLeuGluCysLeuSerGlyGlyGluLeuPheThrHisLeuGluArgGly 177
DB 425 TACCTGTGTGTTGAGAGATGCGGGAGAGCTCCATCTCGAGCCACATCCCAAGACCGCG 484
QY 178 IlePheLeuGluAspThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHis 197
DB 485 CACTTCAACAGAGCTGAGGCGCAGCGTGTGTGAGAGACGTGGCAGCGCTTGAGACTTT 544
QY 198 LeuHisSerGlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSer 217
DB 545 CTGCATACCAAGAGCATGCGCCACAGGAGCATTAAGCCGAGAAACATCTCTGTAGAGAC 604
QY 218 GlnGlyHis-----IleLysLeuThrAspPheGlyLeu----- 228
DB 605 CCCAACAGAGCTTCCCGCGAGATCTGTGACTTCCAGCTGGGAGCGGACATCAAACTC 664
QY 229 -----CysLysGluSerIleHisGluGlyAla-ValThrHisThrPheCysGly 245
DB 665 AACGGGAGCTGCTCCCTAT-CTCCACCCCGAGCTGCTCACTCCG-----TGGGCTC 717
QY 245 rIleGluTyrMetAlaProGluIle----- 253
DB 718 GAGCGAGTACATGCGCCGAGGATGTGAGAGCTTCAGAGAGAGGCTAGACTACGA 777
QY 254 -----LeuValArgSerGlyHisAs 260
DB 778 CACGCGCTGCGAGCTGTGAGAGCTGGCGCTGATCTGTATATATCTACTACGCGCTACCC 837
QY 260 nArgAlaValAsp---TyrPheSer-----LeuGlyAlaLeuMetTyrAspMetIle 276
DB 838 GCCCTTGCGGGCGCGTGTGGAGAGCACTGGCGCTGGAGCCGCTGATGTAGACATGCT 897
QY 276 uThrGlySerProPheThrAlaGluLeuArgLygLygThrMechAspLysIleIleArg 296
DB 898 CACTGAGTCCCGCGCTTTCACCGAGAACCGGAGAAACCAATGATTAAGTCACTCAG 957
QY 296 gGlyLysLeuAlaLeuProTyrLeuThrProAspAlaArgAspLeuValLysLysPhe 316
DB 958 GGGCAACTGGCACTNCCCTTACCTCAACCCAGAGTCCCGGAGCTTGTCAAAAAGTT 1017
QY 316 eLeuLysArgAsnProSerGlnArgIleGlyGlyPheGlyAspAlaAlaAspValGlu 336

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DB 1018 TCTGAACGAGATCCAGCCAGGCAATTGGGGGTGGCCAGGGGAGTCTGTAGTGC 1077
QY 336 nArgHisProPheArgHisMetAsnTrpAspIleLeuAlaTyrArgValAspPr 356
DB 1078 GAGACATCCCTTTTTCGCGACATGATTTGGAGACGACTTTCGCGCTGCGCGTGGACCC 1137
QY 356 oProPheArgProCysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPhe 376
DB 1138 CCGTTTCAAGCGCTGTCTCTCAGTCAAGAGAGACGAGACGATTTGATACCGCTTTCAC 1197
QY 376 rArgGlnThrProValAspSerProAspAspThrAlaLeuSerGluSerAlaAsnGlnAl 396
DB 1198 ACGGACAGCGCGGTGGACAGTCTGTATGACACAGCCCTCAGCGAGAGGCCAACAGAGC 1257
QY 396 aPheLeuGlyPheThrTyrValAlaProSerValLeuAspSerIleGlyGlnGlyPhe 416
DB 1258 CTTCCTGGCTTCACTACGTGAGCGCGCTCTCTCGACACATCAAGAGGAGCTTTC 1317
QY 416 rPheGlnProLysLeuArgSerProArgArgLeuAsnSerProArgValProValSe 436
DB 1318 CTTCAGCCAGGAGTGCCTCAACAGGCGCTCAAGATAGCCCGCGGTCCCGTCAAG 1377
QY 436 rProLeuLysPheSerProPheGlnGlyPheArgProSerProSerLeuProGluPro 456
DB 1378 CCCCCCAAGTTCTCCCTTTTGAAGGGGTTTGCGCCAGCCCAAGCTGCGGAGGCCAC 1437
QY 456 rGluLeuProLeuProProLeuLeuProProProProSerThrAlaProLeuPr 476
DB 1438 GAGGCTACTTCACTTCACTTCTGCAACCGCGCGCTGACCAACCGCCCTTCCC 1497
QY 476 oIleArgProProSerGlyThrLysSerLysArgGlyArgGlyArgProGlyArg 495
DB 1498 CATCCGTCGCCCTCCGAGGAGCAAGAGTCAAGAGGAGCGCTGGGCGCTCGAGGGCGT 1555

RESULT 6
US-09-016-434-118
Sequence 118, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OR INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OR INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016.434
FILING DATE: HEREWITH
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeiler, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:

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; LENGTH: 669 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT11
; CLONE: 1290913
;
US-09-016-434-118

Alignment Scores:
Pred. No.: 1,29e-72 Length: 669
Score: 942.00 Matches: 204
Percent Similarity: 90.71% Conservative: 1
Best Local Similarity: 90.27% Mismatches: 19
Query Match: 36.04% Indels: 7
Gaps: 1

US-09-762-258-2 (1-495) x US-09-016-434-118 (1-669)

QY 5 ArgArgAlaArgGlyAlaGlyAlaAlaMetAlaAlaValPheAspLeuAspLeuGluThr 24
Dd 2 CGACGGGCGCGCGGGGGGCGGCGCGCCGACATCGCGCGCGTGTGATTGATTTGATTTGACAGCG 59
QY 25 GluGluGluLeuSerGluGluGluGluGluGluProGluLeuSerProAlaAspAlaCysProLeu 44
Dd 60 GAGGAAAGCGACGAGGGGCGAGGGCGAGCCGACCTTAACNCCGCGACGACATGTCCTT 111
QY 45 AlaGluLeuLeuArgAlaAlaGlyLeuGluProValGlyHisTyrGluValGluLeuThr 64
Dd 120 GCCAGATTGAGGGGAGCGAGCTGCGCTCAGAGCCGTGTGGACATAGAA-----GAGGGACT 177
QY 65 GluThrSerValAsnValGlyProGluArgIleGlyProHisCysPheGluLeuLeuArg 84
Dd 173 GAGACCGACGCGTGAACGTTGGCCCGACAGCGCATCGGGCCCCACTGCTTGAAGCTGCGGT 233
QY 85 ValLeuGluGlyGluGlyGlyTyrGlyLysValPheGluValArgLysValGluGlyThrAsn 104
Dd 233 GTGCTGGCGCAGGGGGGCGTATGGCAAGGTGTTCAGAGCGAANAGTGCAAGGCAAC 297
QY 105 LeuGluGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLys 124
Dd 293 TTGGGCAAAATATATATGCGCATGAAAGTCTTAAGGAAGGCCAAATATGTGGCAATGCCAAG 355
QY 125 AspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIle 144
Dd 353 GACACACACACACACCGGCTGAGCGCAACATTTAGAGCTAGTAAGACACCCCTTAAT 411
QY 145 ValGluLeuLeuAlaTyrAlaPheGluThrGlyGlyLysLeuTyrLeuIleLeuGluCysLeu 164
Dd 413 GTGGAANAGGCCATATGCTTCCAGACATGGTGGGAACCTTACCACATCTTAGAGTCC 477
QY 165 SerGlyGlyLeuLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAla 184
Dd 473 AGTGTGGCCACGCTTTCACGCAATCGGAGCAGAGGGGCAATCTTCTCGAAGATACGGCC 533
QY 185 CysPheTyrLeuLeuGluIleThrLeuAlaLeuGlyHisLeuHisSerGluGlyIleIle 204
Dd 533 TGTTTCATACGAGCTAGATACAGCTGGCGCTGGGCGCATCTCACTCCAGGGCATATC 599
QY 205 TyrArgAspLeuLysProGluAsnIleLeuSerSerGluGlyHisIleLysLeuThr 224
Dd 591 TACCGGAGACTCAAGCCCGAGACATCATGCTCAGAGCAGAGGCGACATCAACTGANC 655
QY 225 AspPheGlyLeuCysLys 230
Dd 651 GAAATTGGACTCTGCAAG 668

RESULT 7
US-09-031-295-1
; Sequence 1, Application US/09031295
; Patent No. 6326181
; GENERAL INFORMATION:
; APPLICANT: LANS, Florian

```

```

1 APPLICANT: WALDEGGER, Tubigen
2 TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
3 NUMBER OF SEQUENCES: 4
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: FOLEY & LARDNER
6 STREET: 3000 K Street, N.W.
7 CITY: Washington
8 STATE: D.C.
9 COUNTRY: U.S.A.
10 ZIP: 20007-5109
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: PatentIn Release #1.0, Version #1.30
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/09/031,295
19 FILING DATE: 26-FEB-1998
20 CLASSIFICATION: 435
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: DE 197-08-173.8
23 FILING DATE: 28-FEB-1997
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Sandercock, Colin G.
26 REGISTRATION NUMBER: 31,298
27 REFERENCE/DOCKET NUMBER: 058315/0123
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (202) 672-5300
30 TELEFAX: (202) 672-5399
31 INFORMATION FOR SEQ ID NO: 1:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 2370 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: single
36 TOPOLOGY: linear
37 MOLECULE TYPE: cDNA
38 FEATURE:
39 NAME/KEY: CDS
40 LOCATION: 43..1335
41 US-09-031-295-1
42
43 Alignment Scores:
44 Pred. No.: 4,16e-60 Length: 2370
45 Score: 806.50 Matches: 172
46 Percent Similarity: 61.348 Conservative: 66
47 Best Local Similarity: 44.338 Mismatches: 111
48 Query Match: 30.854 Indels: 39
49 DB: 4 Gaps: 12
50
51 US-09-762-258-2 (1-495) x US-09-031-295-1 (1-2370)
52
53 33 GlnProGluIleuSerProAlaAspAlaCysProLeuAlaGluIleuArgAlaAlaGlyLeu 52
54 235 GAGCTCGAGACTTATGATGATCCCAACCTTCTCTCT-----267
55 53 GlnProValGlyHisIleGluGluValAlaIleuThrGluThrSerValAsnValGlyPro 72
56 268 ---CCACCAAGTCTCTTCAGCAA-----ATCAACCTTGGCCG 303
57 73 GluArgIleGlyProHisCys-----PheGluIleuLeuArgValIleuGlyLys 88
58 304 TCGTCC---AATCCCAATGCTAAACATCTGACCTTCACTTCTGAAGAAGTATCGGAAG 360
59 89 GlyGlyTyrGlyIleValPheGluValArg---LysValGlnGlyThrAsnLeuGlyLys 107
60 361 GGGAGTCTTTGGAAAGGTTCTTACAGCAAGACAAAGGAGAGAGAG---408
61 108 IleTyrAlaMetIleValIleuArgIleValLysIleValArgAsnAlaLysAspThrAla 127
62 409 TTGTATGAGAGTCAAAAGTTTACAGAGAAAGAAACAATCTGAAAAAG---AAAGAGAGAGAG 465
63 128 HisThrArgAlaGluArgAsnIle---LeuGluSerValIleHisProPheIleValGlu 146
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Db	466	CATATTATGTCGACCGGATGTTCTGTTGAAGAAATGTGAACACCCCTTCTGCTGATG936C	525
Qy	147	Leu1aaryAlaIaphGdlrThrcIyglyIysIeuYrIleu1IleuIdlucyIseuSergly	166
Db	526	CTTCACTCTCTCTTCCTGAGCTGCTGACAAATATGACTTTTCTTGACTGACATTAATG3T	585
Qy	167	GlyIulePheThrHisIseuGluArgIugIyIlePheIeugIuAspThrAlaCysPhe	186
Db	586	GGAGAGTGTGTTCTACCATCTCCAGAGGGAACCGTGGTCTTGAAACACAGGGCTGTTTC	645
Qy	187	TyrIleuAlaGluIleThrIleuAlaIeugIyHisIseuHisSerGInglyIleIleYrArg	206
Db	646	TATGCTGCTGAATGAGCCAGTGCCTTGGCTACCTGCATCTCACTGACATCCATTATAGA	705
Qy	207	AspIeUysProGluAsnIleMetIeuSerSergInglyHisIleUysIeuThrAspHe	226
Db	706	GACTTAAACCGAGAAATATTTTGTCTAAGTATCACAGGACACATTTGCTTACTATATTC	765
Qy	227	GlyIeuCysIysGluSerIleHisGluGlyAlaValIThrHisThrPheCysGlyThrIle	246
Db	766	GGACTCTGCAGAGAAACATTGAACAACAACACACATCCACTTCTGTGTGGACGGC	825
Qy	247	GluYrMetAlaProGluIleUeuValArgSerGlyHisAsnArgAlaValAspThrTrp	266
Db	826	GAGTATCTCGACCTGAGGTCTTCAATAGCAGCCCTTATGACAGACATGTGACTGATG93	885
Qy	267	SerIeuGlyAlaIeuMetTyrAspMetIeuThrGlySerProProPheThrAlaGluAsn	286
Db	886	TGCCTGGAGAGCTGCTGTATAGATATGCTGTATGCGCTGCGCCCTTTTATAGCGGAAAC	945
Qy	287	ArgIyIysIThrMetAspIysIleIleArgGlyIysIleuAlaIeuProGlyIeuThr	306
Db	946	ACAGCTGAAATGTACGACACATTCCTGAAACAGCCCTTCCACCTCAACCAATATTAACA	1005
Qy	307	ProAspAlaArgAspIeuValIysIysPheIeuYsArgAsnProSerGlnArgIleGly	326
Db	1006	AATTCGCGAAGCACCTCTCGAGGGCCCTCTCGCAAGACAGACAAAGGGCTC---	1065
Qy	327	GlyIyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisIserAsnTrp	346
Db	1063	GGGGCGCAAGATGATCTCATGAGAGATTAAGTCAATGCTTCTTCTTATTAATCGG	1122
Qy	347	AspAspIleuIleuAlaTrpArgValAspProProPheArgProCysIeuGlnSerIeuGlu	366
Db	1123	GATGATTCATTAATAAGACAGATTACTCCCTTTTAAACCAATGATGATGGGCCCAAC	1182
Qy	367	AspValSerGlnPheAspThrArgPheThrArgGlnThrProVal-----	381
Db	1183	GAGCTACGACACTTTGACCCCGAGTTTACCGGAAG---CGTGTCCCAACATCCATGTGGC	1233
Qy	382	AspSerProAspAsp-----ThrAlaIeuSerGluSerAlaAsnGlnAlaPheIeu	398
Db	1240	AAGTCCCTCGACAGGCTCCTGTCACACGACAGCAAGAGAGAGCTGCGAGGGCTTTCCTA	1295
Qy	399	GlyPheThrYrValAlaProSer 406	
Db	1300	GGCTTTTCTATGCGCTCCACG 1323	
RESULT 8			
US-08-712-709-6			
; Sequence 6, Application US/08712709			
; Patent No. 5863780			
GENERAL INFORMATION:			
APPLICANT: Au-Young, Janice			
APPLICANT: Guegler, Karl J.			
APPLICANT: Hawkins, Phillip R.			
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES			
NUMBER OF SEQUENCES: 9			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Incyte Pharmaceuticals, Inc.			
STREET: 3174 Porter Drive			
CITY: Palo Alto			
STATE: CA			

```

COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2311 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
LIBRARY:
IMMEDIATE SOURCE:
CLONE: Consensus
US-08-712-709-6

Alignment Scores:
Pred. No.:      8,88e-60      Length:      2311
Score:          802.50       Matches:     172
Percent Similarity: 61.08%   Conservative: 65
Best Local Similarity: 44.33% Mismatches:    112
Query Match:     30.70%     Indels:      39
DB:              2           Gaps:        12

US-09-762-258-2 (1-495) x US-08-712-709-6 (1-2311)
QY      33  GluProGluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArgAlaAlaGlyLeu 52
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QY      53  GluProValGlyHisIleArgLuuValGluLeuThrGluInrServAlaAsnValGlyPro 72
Db      235 ---CCACCAGAATCTTTCAGCAA-----ATCAACTTGCCCG 270
QY      73  GluArgGleArgProHisCys-----PheGluLeuLeuArgValLeuGlyLys 88
Db      271 TGTGTC---AATCTCATGCTAAACCATCTGACTTCACTTCTGAAGTAGATGGAAAG 32
QY      89  GlyGlyTYrGlyLysValPheGlnValArg--LysValGlnGlyThrAsnLeuGlyLys 107
Db      328 GGGAGTTTGGAAAAGGTTCTCTACAGACACAGAGGAGCAAGAGTG----- 373
QY      108 IleTYrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAspThra 127
Db      376 TTCTATGACGTCAAAAGTTTTACAGAGAAAGCAATCTGAAAAAG---AAAGAGAGAG 433
QY      128 HisThrArgAlaGluArgAsnLe--LeuGlnSerValLysHisproPheIleValGlu 146
Db      433 CATATATATGCGGAGGAGGAATGTTCTGTGAAGATGGAAGCACCCCTTCTCGTGGGC 492
QY      147 LeuAlaTYrAlaPheGlnIleArgLysLysLeuTYrLeuIleLeuGluCysLeuSerGly 166
Db      493 CTTCACCTTCTCTTCCAGCTGCTGACAATAATGTACTTGTCTCTGACTACATTAAATGT 555
QY      167 GlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThraLysPhe 186
Db      553 GGAGATTTGTTTACCATCTCCAGAGGGAGACCGTCTTCTGGAACACAGGGCTCGTTCC 612
QY      187 TYrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTYrArg 206

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613 TATGCTGTAATAAGACAGAGCTTGGGCTACCTGATTCATGACATGACATGCTTTATAGA 672
QY AspleuLysProGluAsnIleMetLeuSerGlnGlyHisIleLysLeuThrAspPhe 226
673 GACTTAAACAGAGAAATATTTTGTATATTCACAGGAGACATGTCCTTACTGACACTTC 732
QY GlysLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIle 246
733 GGACTCTGCAAGAGAACATGACATGACACACACACACACATCCACTCTGTGGCAGCGCC 792
QY GluThrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTrp 266
793 GAGTATCTCGACACGAGCTCTTCATAGACAGCTTATGACAGACGTGAGCTGAGCTGG 852
QY SerLeuGlyAlaLeuMetThrAspMetLeuThrGlySerProProPheThrAlaGluAsn 286
853 TGCCTGGAGCTGCTTGTATGAGATGCTGTATGAGCTGCGCGCTTTTATAGCGGAAC 912
QY ArgLysLysThrMetAspLysIleIleArgLysLysLeuAlaLeuProProTrpLeuThr 306
913 ACAGCTGAATGTACGACACATTCCTGAACAGCCTCTCCAGCTGAACCAATATATACA 972
QY ProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArgIleGly 326
973 AATCCGAGACACACCTCTCTGAGGCGCTCTCTGAGAGACAGACACAAACGCGCTC 1029
QY GlyGlyProGlyAspAlaAlaAspValGlnArgHisProPheArgHisMetAsnTrp 346
1030 GGGGCGAAGATGATCTTCATGAGATGATGAGATGATGATCTTCTTCTTATATATGCTGG 1089
QY AspAspLeuLeuAlaTrpArgValAspProProPheArgProCysLeuGlnSerGlnGlu 366
1090 GATATCTCATATATTAAGAGATTAATCTCCCTTTAAACCAATGTAGTGGGCCCAAC 1149
QY AspValSerGlnPheAspThrArgPheThrArgGlnThrProVal 381
1150 GACCTACGCGACCTTTCAGCCGAGTTTACCGAAGG---CCTGTCGCCCACTCATTCAGC 1206
QY AspSerProAspAsp-----ThrAlaLeuSerGlnSerAlaAsnGlnAlaPheLeu 398
1207 AAGTCCCTGACAGCGTCTGTCAGCGCCAGCGTCAAGAGAGTGGCGAGGCTTTCTTA 1266
QY GlyPheThrTrpValAlaProSer 406
1267 GGCCTTTCCTATGCGCCTCCACG 1290

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RESULT 9  
 US-09-111-444-6  
 Sequence 6, Application US/09111444  
 Patent No. 6045792  
 GENERAL INFORMATION:  
 APPLICANT: Au-Young, Janice  
 APPLICANT: Guegler, Karl J.  
 APPLICANT: Hawkins, Phillip R.  
 TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Inocyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: U.S.  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSO Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/111,444  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/712,709

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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2311 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-09-111-444-6
Alignment Scores:
Pred. No.: 8,88e-60 Length: 2311
Score: 802.50 Matches: 172
Percent Similarity: 61.08% Conservative: 65
Best Local Similarity: 44.33% Mismatches: 112
Query Match: 30.70% Indels: 39
DB: 3 Gaps: 12
US-09-762-258-2 (1-495) x US-09-111-444-6 (1-2311)
QY 33 GluProGluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArgAlaAlaGlyLeu 52
DB 202 GACCTGAGGCTTATGATGATGACCAACCTTCTCT-----ATCAACCTTGGCGCG 234
QY 53 GluProValGlyHisTrpGluGluValGluLeuThrGluThrSerValaAsnValGlyPro 72
DB 235 ---CCACCAAGTCTTCTTCAGCA-----ATCAACCTTGGCGCG 270
QY 73 GluArgIleGlyProHisCys-----PheGluLeuLeuArgValaLeuGlyLys 88
DB 271 TCGTCC---AATCTGATGCTAAACATGACTGACTTTCACCTCTTGAAGATGCGAAG 327
QY 89 GlyGlyTrpGlyLysValaPheGlnValArg---LysValaGlnGlyThrAsnLeuGlyLys 107
DB 328 GGCAGTTTGGAAAGGTTCTTTCAGCAAGACACAGCAAGAGAGAGT----- 375
QY 108 IleThrAlaMetLysValaLeuArgLysAlaLysIleValaArgAsnAlaLysAspThrAla 127
DB 376 TTCTATGAGCTCAAGGTTTACAGAGAAAGCAATCTGAAAAG---AAGAGGAGAG 432
QY 128 HisThrArgAlaGluArgAsnIle---LeuGlnSerValaLysHisProPheIleValaGlu 146
DB 433 CATATATATGCGAGGAGGATGTTCTGTGAAGAAAGTGAAGACCCCTTCTGTGGCG 492
QY 147 LeuAlaThrAlaPheGlnThrGlyGlyLysLeuTrpLeuIleLeuGlnCysLeuSerGly 166
DB 493 CTTCACCTCTCTTCCAGACGCTGTCACAAATGTACTTGTCTTCACTCACTCAATAGT 552
QY 167 GlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCysPhe 186
DB 553 GAGAGTTTGTTCACATCTCCAGAGGGAACGCTGCTTCTGGAACCAAGGCTCGTTCC 612
QY 187 TyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTrpArg 206
DB 613 TATGCTGTAATAAGACAGAGCTTGGGCTACCTGATTCATGACATGCTTTATAGA 672
QY 207 AspleuLysProGluAsnIleMetLeuSerGlnGlyHisIleLysLeuThrAspPhe 226
DB 673 GACTTAAACAGAGAAATATTTTGTATATTCACAGGAGACATGTCCTTACTGACACTTC 732
QY 227 GlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIle 246
DB 733 GGACTCTGCAAGAGAACATGACACACACACACACATCCACTCTGTGGCAGCGCC 792

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QY 247 GlnTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyrTrp 266  
 DB 793 GAGTATCTCGACCTGAGGCTCTCATTAAGAGCTGAGCTGCTGG 852  
 QY 267 SerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProPheThrAlaGluAsn 286  
 DB 853 TGCTGGAGAGCTGCTGTATGAGATCTGTATGCGCTGCGCTTTTATACCGAAC 912  
 QY 287 ArgLysIysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProTyrLeuThr 306  
 DB 913 ACACCTGAATGTACGACCAATCTGACACAGCCCTCCAGCTGAACCAATATTACA 972  
 QY 307 ProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArgIleGly 326  
 DB 973 AATCCCGACAGACCTCTCGAGGCGCTCTCGAGAGACAGACAGACAGCGCTC--- 1029  
 QY 327 GlyGlyProGlyAspAlaAlaAspValGlnArgHisProPheArgHisMetAsnTrp 346  
 DB 1030 GGGGCAAGATGACTTCATGAGATTAAGATCATGTCTTCTTCTTAAATTAACTGG 1089  
 QY 347 AspAspLeuLeuAlaTyrArgValAspProProPheArgProCysLeuGlnSerGluGlu 366  
 DB 1090 GATGATCTCATTAATTAAGAGATTAATCTCCCTTTTAAACCAATGTAGTGGGCCAAC 1149  
 QY 367 AspValSerGlnPheAspThrArgPheThrArgGlnThrProVal----- 381  
 DB 1150 GACTTACGAGACCTTGAACCCGAGTTTACGAGAG---CTGTCCCAACTCCATTGGC 1206  
 QY 382 AspSerProAspAsp-----ThrAlaLeuSerGlnSerAlaAsnGlnAlaPheLeu 398  
 DB 1207 AAGTCCCTTACAGCGCTCTCGTACAGCGAGCGTCAAGAGATGCGAGGCTTCTTCT 1266  
 QY 399 GlyPheThrTyrValAlaProSer 406  
 DB 1267 GCGTTTCTTATGCGCTCCACAG 1290  
 RESULT 10  
 US-09-541-228-6  
 ; Sequence 6, Application US/09541228  
 ; Patent No. 6232077  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Guegler, Karl J.  
 ; APPLICANT: Hawkins, Phillip R.  
 ; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: U.S.  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/541,228  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/712,709  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0118 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-855-0555  
 ; TELEFAX: 415-845-4166  
 ; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2311 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY:  
 ; CLONE: Consensus  
 ; US-09-541-228-6  
 Alignment Scores:  
 Pred. No.: 8,89e-60 Length: 2311  
 Score: 802.50 Matches: 172  
 Percent Similarity: 61.08 Conservative: 65  
 Best Local Similarity: 44.338 Mismatches: 112  
 Query Match: 30,708 Indels: 39  
 DB: Gaps: 12  
 US-09-762-258-2 (1-495) x US-09-541-228-6 (1-2311)  
 QY 33 GlnProGluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArgAlaIleGlyLeu 52  
 DB 202 GAGCCTGAGCTTATGAAATGCAACCTTCTCT----- 234  
 QY 53 GlnProValGlyHisTyrGluGluValGluLeuThrGluThrSerValAsnValGlyPro 72  
 DB 235 ---CAACCAAGCTCTTCAGCA-----ATCAACTTGGCCCG 270  
 QY 73 GluArgIleGlyProHisCys-----PheGluLeuLeuArgValLeuGlyLys 88  
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 DB 328 GCGAGTTTGAAGAGCTTCTTACAGACAGCAAGGAGAGAGT----- 375  
 QY 108 IleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAspThrAla 127  
 DB 376 TTCATGACGTCGAAGATTATTACAGAAAGCAATCTGAAGAG---AAGAGAGAGAG 432  
 QY 128 HistThrArgAlaGluArgAsnIle---LeuGlnSerValLysHisProPheIleValGlu 146  
 DB 433 CATATTATGTCGAGCGAGATGCTTGTGAAGATGAGAGACCCCTTCTGCTGGGCG 492  
 QY 147 LeuAlaTyrAlaPheGlnThrGlyLysLeuTyrLeuIleLeuGluCysLeuSerGly 166  
 DB 493 CTTCACCTTCTTTCACAGCTGCTGACAAATGTACTTGTCTTGACTACATTAATGCT 552  
 QY 167 GlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCysPhe 186  
 DB 553 GAGAGATTGTCTTACCATCTCCAGGAGAGAGCTGCTCTGAAACCAAGGCTGTGTC 612  
 QY 187 TyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTyrArg 206  
 DB 613 TATGCTGCTGAATGACAGAGCTCTGGGCTACGCACTTCACTGAACATGTTATAGA 672  
 QY 207 AspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThrAspPhe 226  
 DB 673 GACTTAAACAGAGAAATATTTGTACATTCACAGGAGACATTTGCTTACTACGACTTC 732  
 QY 227 GlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIle 246  
 DB 733 GAGCTCTGACAGAGAACTTGAACACACAGACACACATCTCCTTCTGTGGACGCG 792  
 QY 247 GlnTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyrTrp 266  
 DB 793 GAGTATCTCGACCTGAGGCTCTCATTAAGAGCTGAGCTGCTGG 852  
 QY 267 SerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProPheThrAlaGluAsn 286  
 DB 853 TGCTGGAGAGCTGCTGTATGAGATCTGTATGCGCTGCGCTTTTATACCGAAC 912

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QY 287 ArglyslvThrMetAspLysIleIleArglyLysLeuAlaLeuProTyrLeuThr 306
DB 913 ACAGCTGAATGTCGACACATTTCTGACCAAGCTCTCCAGCTGAACCAATATTACA 972
QY 307 ProAspAlaArgAspLeuValLysLysPheLeuLysArgAspProSerGlnArgIleGly 326
DB 973 AATTCGCCAGACACCTCTCTGAGGGCTCTCTGACAGAGACAGACAGAAAGGGCTC--- 1029
QY 327 GlyIlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetLeuTyr 346
DB 1030 GGGGCCAGAGATGACTTCATGAGATTAAGAGTATCTCTCTCTCTCTCTCTCTCTCTCT 1089
QY 347 AspAspLeuLeuAlaTyrArgValAspProPheArgProCysLeuGlnSerGlnGlu 366
DB 1090 GATATCTCATTTATTAAGAAATTAATCTCCCTTTTAAACCAATGTAGTGGGCCCAAC 1149
QY 367 AspValSerGlnPheAspThrArgPheThrArgGlnThrProVal----- 381
DB 1150 GACCTACGCGACCTTTGACCCCGAGTTCACGAGAG---CCTGTCCCACTCCATTGCG 1206
QY 382 AspSerProAspAsp-----ThrAlaLeuSerGlnSerAlaSerGlnAlaPheLeu 398
DB 1207 AAGTCCCTGACGCGCTCTGTCACAGCGCTCAAGAGAGCTGCCGAGGCTTCTCTA 1266
QY 399 GlyPheThrTyrAlaAlaProSer 406
DB 1267 GGTCTTCTATGCGCTCCACAG 1290

RESULT 11
US-09-016-434-772
Sequence 772, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 772:
SEQUENCE CHARACTERISTICS:
LENGTH: 2311 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: MMLR2DT01

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CLONE: 477245
US-09-016-434-772
Alignment Scores:
Pred. No.: 8,88e-60
Score: 802.50
Percent Similarity: 61.08%
Best Local Similarity: 44.33%
Query Match: 30,704
DB: 4
Gaps: 12

US-09-762-258-2 (1-495) x US-09-016-434-772 (1-2311)
QY 33 GluProGlnLeuSerProAlaAspAlaCysProLeuAlaGluLeuArgAlaIleGlyLeu 52
DB 202 GAGCTGAGGCTTATGATGATGACCTTCTCTCT----- 234
QY 53 GluProValGlyHisTyrGluGluValGluLeuThrGluThrSerValAsnValGlyPro 72
DB 235 ---CGACCAAGTCTCTCGACAA-----ATCAACTGTGGCCCG 270
QY 73 GluArgIleGlyProHisCys-----PheGluLeuLeuArgValLeuGlyLys 88
DB 271 TCGTCC---AATCCTCATGCTAAACCACTGACTTTCACCTTCTTGAAGATCGAAG 327
QY 89 GlyGlyTyrGlyLysValPheGlnValArg---LysValGlnGlyThrAsnLeuGlyLys 107
DB 328 GCGAGTTTGGAAGAGCTTCTTACGACACACACAGCAGAGAAATG----- 375
QY 108 IleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAspThrAla 127
DB 376 TTCTATGACAGTCAAACTTTACAGAAAGAAATCTCAAAAG---AAGAGGAGAG 432
QY 128 HisThrArgAlaGluArgAsnIle---LeuGlnSerValLysHisProPheIleValGlu 146
DB 433 CATATTATGTCGAGAGGAGATGCTGTGAAAGAAATGAAAGACCTTTCCTGTCGGC 492
QY 147 LeuAlaTyrAlaPheGlnThrGlyLysLysLeuTyrLeuIleLeuGlnCysLeuSerGly 166
DB 493 CTTCACCTCTCTTCCAGACTGCTGCAAAATGTACTTGTCTCAATCACTAATATGAT 552
QY 167 GlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGlnAspThrAlaCysPhe 186
DB 553 GAGAGTTTGTACCATCTCCAGAGGAGACCTGCTCTGAAACCAAGGCTCTTCC 612
QY 187 TyrLeuAlaGluIleThrLeuAlaLeuGlnLysIleSerGlnGlyIleTyrArg 206
DB 613 TATGCGCTGAATATGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 672
QY 207 AspLeuLysProGlnAsnIleLeuLeuSerSerGlnGlyHisIleLysLeuThrAspPhe 226
DB 673 GACTTAAACCAAGAAATTTTGTGATGACAGGACAAATGTCCTTACTGACTTC 732
QY 227 GlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisPheCysGlyThrIle 246
DB 733 GACTCTGCAAGAGAACTTGAACACACAGACACACATCCACTCTCTGCGACGCG 792
QY 247 GluTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyrTyr 266
DB 793 GAGTATCTCGACACTGAGGTGCTCATAGACAGCTTATGACAGACTGACGTGG 852
QY 267 SerLeuGlyAlaLeuMetLysPheLeuThrArgLysSerProPheThrAlaGluAsn 286
DB 853 TGCCTGAGAGCTGCTGTGATGAGATGCTGATGAGCTGCGCCCTTTTATGACCAAC 912
QY 287 ArglyslvThrMetAspLysIleIleArglyLysLeuAlaLeuProTyrLeuThr 306
DB 913 ACAGCTGAATGTCGACACATTTCTGACCAAGCTCTCCAGCTGAACCAATATTACA 972
QY 307 ProAspAlaArgAspLeuValLysLysPheLeuLysArgAspProSerGlnArgIleGly 326
DB 973 AATTCGCCAGACACCTCTCTGAGGGCTCTCTGACAGAGACAGACAGAAAGGGCTC--- 1029

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QY 327 GlyGlyProGlyAspAlaIAspValGlnArgHisProPheArgHisMetAsnTrp 346
DB 1030 GGGGCCAAGCATCTTCATGAGATTAAAGATCATGCTCTTCTCTTAATAAATGAG 1089
QY 347 AspAspLeuLeuIleTpaArgValAspProProPheArgProCysSerGlnSerGln 366
DB 1090 GATGATCTCTTAAATAAGAGATTACTCCCTTTTAAACCAATGATGATGAGGCCAAC 1149
QY 367 AspValSerGlnPheAspThrArgPheThrArgGlnThrProVal 381
DB 1150 GACCTACGACCTTTCACCCGAGTTTACCGAAGAG---CTGTCCCAACCTCCATTGAC 1206
QY 382 AspSerProAspAsp-----ThrAlaLeuSerGlnSerAlaSerGlnAlaPheLeu 398
DB 1207 AAGTCCCTTACAGCTCTCTCTACAGCGCATGAGAGAGAGAGAGAGAGAGAGAGAG 1266
QY 399 GlyPheThrTyrValAlaProSer 406
DB 1267 GGCCTTTTCTATGCGCTCCACAG 1290

RESULT 12
US-09-256-465-1
; Sequence 1, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RFS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)..(1533)
US-09-256-465-1

Alignment Scores:
Pred. No.: 1,41e-59 Length: 1599
Score: 797.50 Matches: 168
Percent Similarity: 59.85% Conservative: 69
Best Local Similarity: 42.42% Mismatches: 130
Query Match: 30.51% Indels: 29
DB: Gaps: 8

US-09-762-258-2 (1-495) x US-09-256-465-1 (1-1599)
QY 48 ArgAlaAlaGlyLeuGlnProValGlyHis-----TyrGlnGln 60
DB 424 CGGGCCCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 483
QY 61 ValGlnLeuThrGlnThrSerValAsnValGlyProGlnArgGlyLeuProHisCysPhe 80
DB 484 ACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
QY 81 GlnLeuLeuArgValLeuGlyLeuGlyValGlyTyrGlyValValPheGlnValArgValVal 100
DB 544 GACTATCTCAAACTCTTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 101 GlnGlyThrAsnLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleVal 120
DB 601 -----AAGGCCACTGGCGGCTACTAGCCCATAGATCTGCGAAGAGAGATCATATT 654
QY 121 ArgAsnAlaLysAsp---ThrAlaHisThrArgAlaGlnArgAsnIleLeuGlnSerVal 139
DB 655 -----GCCAAGAGATGAAGTCCCTTCACAGCTACAGAGAGAGAGAGAGAGAGAGAG 708
QY 140 LysHisProPheIleValGlnLeuAlaTyrAlaPheGlnThrGlyLysLeuTyrLeu 159
DB 1599 LysHisProPheIleValGlnLeuAlaTyrAlaPheGlnThrGlyLysLeuTyrLeu 1599

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DB 709 AGGCACCCGTTCTCTACTGCGCTGAAGTATGCTTCCAGACCCAGACCGCTGTCTTT 768
QY 160 IleLeuGlyCysLeuSerGlyValGlnLeuPheThrHisLeuGlnArgGlnGlyIlePhe 179
DB 769 GATATGAGATATGCCAAGCGGGGTGAGCTGTCTTCCACCTGTCCCGGAGAGGTGTCTTC 828
QY 180 LeuGlnAspThrAlaCysPheTyrLeuAlaGlnIleThrLeuAlaLeuGlyHisIleHis 199
DB 829 ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 888
QY 200 SerGlnGlyIleIleTyrArgAspLeuLysProGlnAsnIleMetLeuSerSerGlnGly 219
DB 889 TCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 948
QY 220 HisIleLysLeuThrAspPheGlyLeuGlyCysLysGlnSerIleHisGlnGlyValAlaThr 239
DB 949 CACATCAAGATCACTGACTTTCCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1008
QY 240 HisThrPheCysGlyThrIleGlyTyrMetAlaProGlnIleLeuValArgSerGlyHis 259
DB 1009 AAAACCTTCTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1068
QY 260 AsnArgAlaValAspTyrTrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySer 279
DB 1069 GCGCCGCGCGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1128
QY 280 ProProPheThrAlaGlnAsnArgLysThrMetAlaLysIleLeuArgGlyLysLeu 299
DB 1129 CTGCGCTTCTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1188
QY 300 AlaLeuProProTyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArg 319
DB 1189 CGCTTCCCGCGAGCTGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1248
QY 320 AsnProSerGlnArgIleGlyValGlyProGlyLeuAlaAspValGlnArgHisPro 339
DB 1249 GAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1308
QY 340 PhePheArgHisMetAsnTrpAspLeuLeuAlaTpaArgValAspProProPheArg 359
DB 1309 TTCTTCTCAGCATCACTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1368
QY 360 ProCysLeuGlnSerGlnGlnAspValSerGlnPheAspThrArgPheThrArgGln 378
DB 1369 CCTCAGCTCAGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1428
QY 379 -----ThrProValAspSerProAspAspThrAlaLeuSerGlnSerAlaSerGln 395
DB 1429 ATCACAATCAACACCCCTGACCGCTATGACAGCTGAGCTTACTGAGAGAGAGAGAGAG 1488
QY 396 Ala-----PheLeuGlyPheThrTyr-----ValAlaPro--- 405
DB 1489 ACCCACTTCCCGGAGTCTCTACTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1548
QY 405 -----SerValLeuAspSerIleLysGlnGlyPheSerPheGlnPro 419
DB 1549 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1596

RESULT 13
US-09-167-322-3
; Sequence 3, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA

```







1	2596	99.3	502	12	US-10-435-114-54060	Sequence 54060, App
2	1756	67.2	333	12	US-10-217-155A-16	Sequence 16, App
3	1756	67.2	333	15	US-10-217-574-16	Sequence 16, App
4	1756	66.8	333	15	US-10-217-555-16	Sequence 16, App
5	1740	66.6	502	14	US-10-316-253-32	Sequence 32, App
6	1740	66.6	525	14	US-10-316-253-34	Sequence 34, App
7	1428	54.6	637	9	US-09-817-310-02	Sequence 2, Appl
8	1303	49.8	272	12	US-09-925-298-663	Sequence 663, App
9	1303	49.8	272	14	US-10-102-805-663	Sequence 663, App
10	1211.5	44.9	281	12	US-10-220-555-13	Sequence 13, App
11	1174.5	44.9	342	12	US-10-425-114-34517	Sequence 34517, App
12	951.5	36.6	544	15	US-10-108-690A-3334	Sequence 3334, App
13	951.5	36.6	740	15	US-10-309-493-5149	Sequence 5149, App
14	949.5	36.3	740	9	US-09-771-161A-265	Sequence 265, App
15	949.5	36.3	740	9	US-09-771-161A-266	Sequence 266, App

16	949	36.3	797	15	US-10-369-493-5148	Sequence 5146, Appl
17	949	36.3	797	15	US-10-369-493-5150	Sequence 5150, Appl
18	937.5	35.9	698	14	US-10-102-1054-2	Sequence 2, Appl
19	916.5	35.1	328	12	US-10-217-155A-15	Sequence 15, Appl
20	916.5	35.1	328	15	US-10-217-57A-15	Sequence 15, Appl
21	916.5	35.1	328	15	US-10-217-55A-15	Sequence 15, Appl
22	903.5	34.6	712	12	US-10-425-114-554270	Sequence 54270, Appl
23	854	32.7	773	14	US-10-112-286-2	Sequence 2, Appl
24	851.5	32.6	455	12	US-10-424-559-177033	Sequence 177033, Appl
25	850.5	32.5	345	12	US-10-425-114-45337	Sequence 43537, A
26	844	32.3	198	12	US-10-240-315-4	Sequence 4, Appl
27	810.5	31.0	388	15	US-10-131-410-104	Sequence 104, Appl
28	810.5	31.0	407	14	US-10-067-977-4	Sequence 4, Appl
29	810.5	31.0	431	9	US-09-881-353-7	Sequence 7, Appl
30	810.5	31.0	431	12	US-10-403-161-2	Sequence 2, Appl
31	810.5	31.0	431	12	US-10-403-161-4	Sequence 4, Appl
32	810.5	31.0	445	14	US-10-067-977-2	Sequence 2, Appl
33	810.5	31.0	526	15	US-10-094-748-1661	Sequence 1661, Appl
34	806.5	30.9	431	14	US-10-000-093-2	Sequence 2, Appl
35	806.5	30.9	431	15	US-10-353-639-12	Sequence 12, Appl
36	804	30.8	436	15	US-10-369-498-22653	Sequence 22653, A
37	802.5	30.7	431	9	US-09-810-808-5	Sequence 5, Appl
38	799.5	30.6	1207	10	US-09-949-029-144	Sequence 144, Appl
39	795.5	30.4	481	12	US-10-217-155A-32	Sequence 32, Appl
40	795.5	30.4	481	15	US-10-394-322A-2	Sequence 2, Appl
41	795.5	30.4	481	15	US-10-217-57A-32	Sequence 32, Appl
42	795.5	30.4	481	15	US-10-217-55A-32	Sequence 32, Appl
43	794.5	30.4	340	12	US-10-217-155A-17	Sequence 17, Appl
44	794.5	30.4	340	15	US-10-217-57A-17	Sequence 17, Appl
45	794.5	30.4	340	15	US-10-217-555-17	Sequence 17, Appl

## ALIGNMENTS

```

RESULT 1
US-10-425-114-54060
/ Sequence 54060, Application US/10425114
/ Publication No. US2004003488A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhu, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven B
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 54060
/ LENGTH: 502
/ TYPE: prt
/ ORGANISM: Homo sapiens
/ FEATURES:
/ OTHER INFORMATION: Clone ID: LIB3081-101-B10_F11.pep
/ US-10-425-114-54060

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Query Match	99.3%	Score 2596;	DB 12;	Length 502;
Best Local Similarity	99.8%	Pred. No. 1.3e-178;		
Matches 491;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0
QY	4	GGRRAGAGAAAATVDLDLLETEGSEGGEBELSPADACPLAEIRAAGLEPVGHYEEVEL	63	
Db	11	GGRRAGAGAAAATVDLDLLETEGSEGGEBELSPADACPLAEIRAAGLEPVGHYEEVEL	70	
QY	64	TTSTNNPBERIGPHCELLPVTLGKRGYGVFQVRKQNGNLKTYAMKYLRAKTVRNA	123	
Db	71	TTSTNNPBERIGPHCELLPVTLGKRGYGVFQVRKQNGNLKTYAMKYLRAKTVRNA	130	
QY	124	KQTATTRARNLLESEVKIPFVLELAAYFQNGKLYLLLECLSGAGLPTHLEREGTLEEDT	183	

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Db 131 KOTAHRAERNTLESKHPIVELAFAFOTGKYLILECLSGSELTLEBEGIFLEBT 190
Qy 184 ACFTLAETTLALGHLHSOGIIYRDLKPENIMLSOGHIKLTDFGLCKESIHEGAVTHFTC 243
Db 191 ACFTLAETTLALGHLHSOGIIYRDLKPENIMLSOGHIKLTDFGLCKESIHEGAVTHFTC 250
Qy 244 GTEYAPAEILVRSNGRAVDWMSLGALMYDMTGSPPPTAERKKTMDKIIRGKALP 303
Db 251 GTEYAPAEILVRSNGRAVDWMSLGALMYDMTGSPPPTAERKKTMDKIIRGKALP 310
Qy 304 YLTPDARDLVKKELKXENPSQRIIGGPGDAADVQRHPPFRHNMWDLAMRVDPPEPCLQ 363
Db 311 YLTPDARDLVKKELKXENPSQRIIGGPGDAADVQRHPPFRHNMWDLAMRVDPPEPCLQ 370
Qy 364 SEEDVQOFTRERFROPVDSPPDTALSESANQAFIGFTYVAVSVDLSIEGFSPOPKLS 423
Db 371 SEEDVQOFTRERFROPVDSPPDTALSESANQAFIGFTYVAVSVDLSIEGFSPOPKLS 430
Qy 424 PRILNNSPVPVPSPLKFSPEGFRPSPLPEPTLPLPELPPPPSTTAPPIRPPSGT 483
Db 431 PRILNNSPVPVPSPLKFSPEGFRPSPLPEPTLPLPELPPPPSTTAPPIRPPSGT 490
Qy 484 KSKRGGRGRGR 495
Db 491 KSKRGGRGRGR 502
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## RESULT 2

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US-10-217-155A-16
Sequence 16, Application US/10217155A
Publication No. US20030065855A1
GENERAL INFORMATION:
APPLICANT: Barford, David
APPLICANT: Yang, Jing
APPLICANT: Hemmings, Brian A
APPLICANT: Cron, Peter D
TITLE OF INVENTION: Kinase Crystal Structures and Methods for
FILE REFERENCE: 44236
CURRENT FILING DATE: 2002-08-14
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2002-05-01
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 333
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Sequence source
US-10-217-155A-16
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Query Match 67.2%; Score 1756; DB 12; Length 333;  
Best Local Similarity 100.0%; Pred. No. 2,4e-118; Indels 0; Gaps 0;  
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RIGPHCFELLRLVLAGKGGYKVFQVRKVOGTNLGKIYAMKVLKRAKIVANAKDTAHTRAER 60
Qy 134 NILSEVRHPIVELAFAFOTGKYLILECLSGSELTLEBEGIFLEDTACFTLAETTL 193
Db 61 NILSEVRHPIVELAFAFOTGKYLILECLSGSELTLEBEGIFLEDTACFTLAETTL 120
Qy 194 ALGHLHSOGIIYRDLKPENIMLSOGHIKLTDFGLCKESIHEGAVTHFTFCGTEYMAPEI 253
Db 121 ALGHLHSOGIIYRDLKPENIMLSOGHIKLTDFGLCKESIHEGAVTHFTFCGTEYMAPEI 180
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Qy 254 LVRSNGRAVDWMSLGALMYDMTGSPPPTAERKKTMDKIIRGKALPPLYLTPDARDLV 313
Db 181 LVRSNGRAVDWMSLGALMYDMTGSPPPTAERKKTMDKIIRGKALPPLYLTPDARDLV 240
Qy 314 KKFLENPSQRIIGGPGDAADVQRHPPFRHNMWDLAMRVDPPEPCLQSEEDVSOQDT 373
Db 241 KKFLENPSQRIIGGPGDAADVQRHPPFRHNMWDLAMRVDPPEPCLQSEEDVSOQDT 300
Qy 374 RFTROTVPVDSPPDTALSESANQAFIGFTYVA 404
Db 301 RFTROTVPVDSPPDTALSESANQAFIGFTYVA 331
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## RESULT 3

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US-10-217-574-16
Sequence 16, Application US/10217574
Publication No. US20040005687A1
GENERAL INFORMATION:
APPLICANT: Barford, David
APPLICANT: Yang, Jing
APPLICANT: Hemmings, Brian A
APPLICANT: Cron, Peter D
TITLE OF INVENTION: Kinase Crystal Structures
FILE REFERENCE: 44237
CURRENT FILING DATE: 2002-12-23
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2002-05-01
PRIOR FILING DATE: 2002-05-01
PRIOR FILING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 333
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Sequence source
US-10-217-574-16
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Query Match 67.2%; Score 1756; DB 15; Length 333;  
Best Local Similarity 100.0%; Pred. No. 2,4e-118; Indels 0; Gaps 0;  
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 74 RIGPHCFELLRLVLAGKGGYKVFQVRKVOGTNLGKIYAMKVLKRAKIVANAKDTAHTRAER 133
Db 1 RIGPHCFELLRLVLAGKGGYKVFQVRKVOGTNLGKIYAMKVLKRAKIVANAKDTAHTRAER 60
Qy 134 NILSEVRHPIVELAFAFOTGKYLILECLSGSELTLEBEGIFLEDTACFTLAETTL 193
Db 61 NILSEVRHPIVELAFAFOTGKYLILECLSGSELTLEBEGIFLEDTACFTLAETTL 120
Qy 194 ALGHLHSOGIIYRDLKPENIMLSOGHIKLTDFGLCKESIHEGAVTHFTFCGTEYMAPEI 253
Db 121 ALGHLHSOGIIYRDLKPENIMLSOGHIKLTDFGLCKESIHEGAVTHFTFCGTEYMAPEI 180
Qy 254 LVRSNGRAVDWMSLGALMYDMTGSPPPTAERKKTMDKIIRGKALPPLYLTPDARDLV 313
Db 181 LVRSNGRAVDWMSLGALMYDMTGSPPPTAERKKTMDKIIRGKALPPLYLTPDARDLV 240
Qy 314 KKFLENPSQRIIGGPGDAADVQRHPPFRHNMWDLAMRVDPPEPCLQSEEDVSOQDT 373
Db 241 KKFLENPSQRIIGGPGDAADVQRHPPFRHNMWDLAMRVDPPEPCLQSEEDVSOQDT 300
Qy 374 RFTROTVPVDSPPDTALSESANQAFIGFTYVA 404
Db 301 RFTROTVPVDSPPDTALSESANQAFIGFTYVA 331
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## RESULT 4



US-10-217-555-16  
 ; Sequence 16, Application US/10217555  
 ; Publication No. US2004009569A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Barford, David  
 ; APPLICANT: Yang, Jing  
 ; APPLICANT: Hemmings, Brian A  
 ; APPLICANT: Cron, Peter D  
 ; TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for  
 ; FILE OF INVENTION: Kinase Activation  
 ; FILE REFERENCE: 44236  
 ; CURRENT APPLICATION NUMBER: US/10/217,555  
 ; PRIOR FILING DATE: 2002-12-05  
 ; PRIOR APPLICATION NUMBER: GB 0119860.5  
 ; PRIOR FILING DATE: 2001-08-14  
 ; PRIOR APPLICATION NUMBER: GB 0209985.1  
 ; NUMBER OF SEQ ID NOS: 40  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 16  
 ; LENGTH: 333  
 ; TYPE: PRT  
 ; ORGANISM: Unknown Organism  
 ; FEATURES:  
 ; OTHER INFORMATION: Description of Unknown Organism: Sequence source  
 ; OTHER INFORMATION: uncertain  
 US-10-217-555-16

Query Match 67.2%; Score 1756; DB 15; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-118;  
 Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 RPSHCEFLRVYKGGYGVYVRYKQVGTNLGKIYAMKYLKAKIVRNADYAHTRAE 133  
 DB 1 RPSHCEFLRVYKGGYGVYVRYKQVGTNLGKIYAMKYLKAKIVRNADYAHTRAE 60  
 QY 134 NILESVMHPIVELANAFQGGKLYLLECLSGELFTHLRSGIFLEBDTACFYLAETL 193  
 DB 61 NILESVMHPIVELANAFQGGKLYLLECLSGELFTHLRSGIFLEBDTACFYLAETL 120  
 QY 194 ALGHLISOGIITVDLPENIMLSSOGHILKIDPGLCKESIHGAVHTTFCSTIY 253  
 DB 121 ALGHLISOGIITVDLPENIMLSSOGHILKIDPGLCKESIHGAVHTTFCSTIY 180  
 QY 254 LVSGHNRADVMSIALMYDMLTSGPPTAENRKKTKMKTIRGKALPPYLTPDARDV 313  
 DB 181 LVSGHNRADVMSIALMYDMLTSGPPTAENRKKTKMKTIRGKALPPYLTPDARDV 240  
 QY 314 KXFLKRNPSQRIQGGGADADVORHPFRHMNDLLARVDPFRPCQSEEDVSGQFT 373  
 DB 241 KXFLKRNPSQRIQGGGADADVORHPFRHMNDLLARVDPFRPCQSEEDVSGQFT 300  
 QY 374 RPTROTVDSPDDTALSANQAFLETTYA 404  
 DB 301 RPTROTVDSPDDTALSANQAFLETTYA 331

RESULT 5  
 US-10-316-253-32  
 ; Sequence 32, Application US/10316253  
 ; Publication No. US20030162706A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Procter & Gamble Company  
 ; APPLICANT: Peters, Kevin  
 ; APPLICANT: Thompson, Larry  
 ; APPLICANT: Wang, Feng  
 ; APPLICANT: Greis, Kenneth  
 ; TITLE OF INVENTION: Angiogenesis Modulating Proteins  
 ; FILE REFERENCE: 8865M  
 ; CURRENT APPLICATION NUMBER: US/10/316,253  
 ; CURRENT FILING DATE: 2002-12-10  
 ; PRIOR APPLICATION NUMBER: US 60/355,295  
 ; PRIOR FILING DATE: 2002-02-08

NUMBER OF SEQ ID NOS: 308  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 32  
 ; LENGTH: 502  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-10-316-253-32

Query Match 66.8%; Score 1746; DB 14; Length 502;  
 Best Local Similarity 70.2%; Pred. No. 2e-117;  
 Matches 344; Conservative 51; Mismatches 75; Indels 20; Gaps 7;

QY 14 MAAPFDLDETEGSGEGEPHSPDADCPLE-LRAALRP-----VGHYEVELTETSY 68  
 DB 1 MAGVFDDIDQDPDASDELE---EGQILNESHQDGVGYEYELAMECEFESETSY 56  
 QY 69 NVGERIGPHCEFLAVLGKGYGVYVRYKQVGTNLGKIYAMKYLKAKIVRNADYAH 128  
 DB 57 NNGEKIRPECEFLAVLGKGYGVYVRYKQVGTNLGKIYAMKYLKAKIVRNADYAH 116  
 QY 129 TRAEVILSVKHPPIVELANAFQGGKLYLLECLSGELFTHLRSGIFLEBDTACFY 188  
 DB 117 TRAEVILSVKHPPIVELANAFQGGKLYLLECLSGELFTHLRSGIFLEBDTACFY 176  
 QY 189 AEITLALGHLISOGIITVDLPENIMLSSOGHILKIDPGLCKESIHGAVHTTFCSTI 248  
 DB 177 AEISMLGHLISOGIITVDLPENIMLSSOGHILKIDPGLCKESIHGAVHTTFCSTI 236  
 QY 249 MAPPEILVSGNRADVMSIALMYDMLTSGPPTAENRKKTKMKTIRGKALPPYLTPD 308  
 DB 237 MAPPEILVSGNRADVMSIALMYDMLTSGPPTAENRKKTKMKTIRGKALPPYLTPD 296  
 QY 309 AADLVKFKLRPSQRIQGGGADADVORHPFRHMNDLLARVDPFRPCQSEEDV 368  
 DB 297 AADLVKFKLRPSQRIQGGGADADVORHPFRHMNDLLARVDPFRPCQSEEDV 356  
 QY 369 SGPDRFTRQTPVDSPPDDTALSANQAFLETTYAPSVLDSIKGFSFQPKLRSPRLN 428  
 DB 357 SGPDRFTRQTPVDSPPDDTALSANQAFLETTYAPSVLDSIKGFSFQPKLRSPRLN 416  
 QY 428 SSPRVVSPKRSPE---GFRSPSLPE-PTLEPLPPLPPPPSTT-----APLPR 478  
 DB 417 GSPRTPVSPKRSPE---GFRSPSLPE-PTLEPLPPLPPPPSTT-----APLPR 476  
 QY 479 PP-SGTKSKX 487  
 DB 477 QNNSGPYKKQ 486

RESULT 6  
 US-10-316-253-34  
 ; Sequence 34, Application US/10316253  
 ; Publication No. US20030162706A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Procter & Gamble Company  
 ; APPLICANT: Peters, Kevin  
 ; APPLICANT: Thompson, Larry  
 ; APPLICANT: Wang, Feng  
 ; APPLICANT: Greis, Kenneth  
 ; TITLE OF INVENTION: Angiogenesis Modulating Proteins  
 ; FILE REFERENCE: 8865M  
 ; CURRENT APPLICATION NUMBER: US/10/316,253  
 ; CURRENT FILING DATE: 2002-12-10  
 ; PRIOR APPLICATION NUMBER: US 60/355,295  
 ; PRIOR FILING DATE: 2002-02-08  
 ; NUMBER OF SEQ ID NOS: 308  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 34  
 ; LENGTH: 525  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-10-316-253-34

Query Match 66.6%; Score 1740; DB 14; Length 525;  
 Best Local Similarity 68.0%; Pred. No. 5.8e-117;  
 Matches 349; Conservative 51; Mismatches 83; Indels 30; Gaps 8;

QY 1 MAQRARAGCAA-----MAVFDDLETEGSGEGEPFELSPADACPLAE-LRA 49  
 DB 1 MRRRRRRDGFYPPDFRHRBAEDMAGVFDDLDQPEDAGSEDELE---EGQQLNSMDH 56  
 QY 50 AGLEP-----VGHSEYELTETSYNVGPERIGPHCFELRLYLGKGYGYQYRKVQGTNL 105  
 DB 57 GCGPPELGMHEHCEKEISTSYNRGPEKRFECFELRLYLGKGYGYQYRKVQGTNL 116  
 QY 106 GKIYANKVLRKAKIVNKKOTAHTRAERNLIESVKKPIVELAYAFQGTQKYLILECIS 165  
 DB 117 GKIFAMKVLKAMIVNKKOTAHTRAERNLIEVKKPFIVDLIYAFQGTQKYLILEYIS 176  
 QY 166 GGELEPHLEREGFLEDTACFYLAETTLALGHASHGIIYRDLKXENIMLSQGHKLTLD 225  
 DB 177 GGELEPHLEREGFLEDTACFYLAETTLALGHASHGIIYRDLKXENIMLSQGHKLTLD 236  
 QY 226 FGJCKESIHEGAVYHTPCGIIIEYMAPELIVRSCHNRAYDWMWSIGALMYDMLTGSPPETAB 285  
 DB 237 FGJCKESIHDGVTHTFCGIIIEYMAPELIVRSCHNRAYDWMWSIGALMYDMLTGAPEPTGE 296  
 QY 286 NRKKTMDKIRGLALPYLTPDARLVYKFLKRNPSORIIGGPGDAADVQRRHPPRRHN 345  
 DB 297 NRKKTMDKIRGLALPYLTPDARLVYKFLKRNPSORIIGGPGDAADVQRRHPPRRHN 356  
 QY 346 WDDLARVDPFPRPCLOSEEDVSOPTFRQTPVDSDDPTALSSANQALGFTYVAP 405  
 DB 357 WDDLARVDPFPRPCLOSEEDVSOPTFRQTPVDSDDPTALSSANQALGFTYVAP 416  
 QY 406 SYLDSIKEGSFQPKLRSPRLNSPRVVSFKTSFPR-----GRRPSLPE-FTLEPL 460  
 DB 417 SYLDSIKEGSFQPKLRSPRLNSPRVVSFKTSFPR-----GRRPSLPE-FTLEPL 476  
 QY 461 PLLPFPSTT-----APLPIRPP-SGTGSKK 487  
 DB 477 ETSGIEQMDVTTSGEASALPIRQPSGPKYKQ 509

RESULT 7  
 US-09-817-310-2  
 ; Sequence 2, Application US/09817310  
 ; Patent No. US20010042254A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stewart, Mary  
 ; APPLICANT: Kozma, Sarah  
 ; APPLICANT: Thomas, George  
 ; TITLE OF INVENTION: Drosophila Melanogaster P70 S6 Kinase  
 ; FILE REFERENCE: 4-20971/A  
 ; CURRENT APPLICATION NUMBER: US/09/817,310  
 ; CURRENT FILING DATE: 2001-03-26  
 ; PRIOR APPLICATION NUMBER: 09/230,247  
 ; PRIOR FILING DATE: 1999-04-16  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 637  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 ; US-09-817-310-2

Query Match 54.6%; Score 1428; DB 9; Length 637;  
 Best Local Similarity 67.2%; Pred. No. 2.1e-94;  
 Matches 279; Conservative 47; Mismatches 81; Indels 8; Gaps 4;

QY 19 DLDLLETSBESBEGEP-ELSPADACPLAEPLRAAGLEPCHYEVELTSTSYNVGPERGP 77  
 DB 17 DLDLLETSBESBEGEP-ELSPADACPLAEPLRAAGLEPCHYEVELTSTSYNVGPERGP 74  
 QY 78 HCFELLRLVYLGKGYGYQYRKVQGTNLGKIYANKVLRKAKIVNKKOTAHTRAERNLIE 137

DB 75 KDFELKXVLGKGYGYQYRKVQGTNLGKIYANKVLRKAKIVNKKOTAHTRAERNLIE 134  
 QY 138 SYKHEPPIYELAVPOTGKTLILECISGGEHFTLEEEGIFLETACTYLAETLALGH 197  
 DB 135 AKHEPPIYELAVPOTGKTLILECISGGEHFTLEEEGIFLETACTYLAETLALGH 194  
 QY 198 LHSOGIIVRDLKXENIMLSQGHKLTLDGJCKESIHEGAVYHTPCGIIIEYMAPELIVRS 257  
 DB 195 LHSOGIIVRDLKXENIMLSQGHKLTLDGJCKESIHEGAVYHTPCGIIIEYMAPELIVRS 254  
 QY 258 GGNRAVDWWSIGALMYDMLTGSPPETABNRKKTMDKIRGLALPYLTPDARLVYKFL 317  
 DB 255 GGNRAVDWWSIGALMYDMLTGSPPETABNRKKTMDKIRGLALPYLTPDARLVYKFL 314  
 QY 318 KNPESQIRIGGPGDAADVQRRHPPRRNMDDLARVDPFPRPCLOSEEDVSOPTFRPTR 377  
 DB 315 KNPESQIRIGGPGDAADVQRRHPPRRNMDDLARVDPFPRPCLOSEEDVSOPTFRPTR 374  
 QY 378 QTPVDSDDPTALSSANQALGFTYVAPSYLDSIKEGSFQPKLRSPRLNSPR 432  
 DB 375 QTPVDSDDPTALSSANQALGFTYVAPSYLDSIKEGSFQPKLRSPRLNSPR 424

RESULT 8  
 US-09-925-298-663  
 ; Sequence 663, Application US/09925298  
 ; Publication No. US20020039764A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA103  
 ; CURRENT APPLICATION NUMBER: US/09/925,298  
 ; CURRENT FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05881  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124,270  
 ; PRIOR FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 846  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 663  
 ; LENGTH: 272  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURES:  
 ; NAME/KEY: SITE  
 ; LOCATION: (129)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; US-09-925-298-663

Query Match 49.8%; Score 1303; DB 12; Length 272;  
 Best Local Similarity 99.6%; Pred. No. 7.7e-86;  
 Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 253 ILVRSCHNRAYDWMWSIGALMYDMLTGSPPETABNRKKTMDKIRGLALPYLTPDARLV 312  
 DB 30 ILVRSCHNRAYDWMWSIGALMYDMLTGSPPETABNRKKTMDKIRGLALPYLTPDARLV 89  
 QY 313 VKKFLKSNPSORIGGPGDAADVQRRHPPRRNMDDLARVDPFPRPCLOSEEDVSOPTFRPTR 372  
 DB 90 VKKFLKSNPSORIGGPGDAADVQRRHPPRRNMDDLARVDPFPRPCLOSEEDVSOPTFRPTR 149  
 QY 373 TRFTRQTPVDSDDPTALSSANQALGFTYVAPSYLDSIKEGSFQPKLRSPRLNSPR 432  
 DB 150 TRFTRQTPVDSDDPTALSSANQALGFTYVAPSYLDSIKEGSFQPKLRSPRLNSPR 209  
 QY 433 VPVSPFLKSPFEGGRSPSPSPPTLEPLPLPPLPSTTAPLPIRPPSGTKSKRGGR 492  
 DB 210 VPVSPFLKSPFEGGRSPSPSPPTLEPLPLPPLPSTTAPLPIRPPSGTKSKRGGR 269  
 QY 493 PGR 495  
 DB 270 PGR 272



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QY 425 RUNSSRVVSPKESP--FEGRRSPSPPELPLPPPPS-----470
DB 253 RRTIGSRIVSPKSPBDFWKGASAS---TANQTVEXYMETSIGEDMTMSGE 308
QY 471 TTAPLPIRP-SGTKSK 487
DB 309 ASAPLPIRPNRSGPYKKQ 326

```

RESULT 12  
US-10-108-260A-3334

Sequence 3334, Application US/10108260A  
Publication No. US20040005560A1  
GENERAL INFORMATION:  
APPLICANT: HELIX RESEARCH INSTITUTE  
TITLE OF INVENTION: No. US20040005560A1 full length cDNA  
FILE REFERENCE: HI-A0106  
CURRENT APPLICATION NUMBER: US/10/108,260A  
CURRENT FILING DATE: 2002-03-27  
NUMBER OF SEQ ID NOS: 5458  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3334  
LENGTH: 544  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-108-260A-3334

Query Match 36.4%; Score 955.5; DB 15; Length 544;  
Best Local Similarity 45.8%; Pred. No. 1,86-60;  
Matches 196; Conservative 74; Mismatches 105; Indels 53; Gaps 9;

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QY 43 PLAL-----RAAGLEPVGHVEVELTETSVA--VGP-----72
DB 2 PIAQLELMWKIIEVEPW---ELETSEEDNLMDVGPATBEDTAESEGVWEIDISHVXK 57
QY 73 --BRIGPHCELLRVYKGGYGVQVQYKQVGTNIGKIYAMKYLAKKIVRNADOTAFNR 130
DB 58 GFKADPSQELKLVAGQSYGVFLVRKVGSDAQGLYAMKYLAKKATL--KVRDVRKX 115
QY 131 AERNILSEVYKPIVYELAVAFQTKGLYLLIECLSGSELETHLEREGIFLEDYACFYLA 190
DB 116 MERDILAEVNHPIVYKLVHAFQTEGSKLYLLIDPLRGDLETRLSKEVMTSEOVKRYLA 175
QY 191 ITALGLHSOGIYYIDKPEINMLSSQGHIXLTDGLCESEIHGAVHTTQCTEYVA 250
DB 176 IALALDLHSLGIYIDKPEINMLLDEGHIXITDRLSGEALDHDRAVSFGTLEYNA 235
QY 251 PELVSGENRAVDWMSIGALMYDMLTGSPPPTAENRKKIMDKIRGKUALPPYLTPDAR 310
DB 236 PEVYVNRGHTQSDAMWSFGVLMFEMLTGSLPFGCKDKRKETMALILAKLGMFGLSGEAQ 295
QY 311 DYKXKPLKRNPSQRIIGGSGDADVDQRHPPFRHMMDDLLAMVDPFRCLQSEEDVQ 370
DB 296 SLIRALFKRNPCRLGAGIDGVEIRKHPPFTIDMTWTLRKIKPFPKAVGPRPDTH 355
QY 371 FDRFTQRTQVDSDDTALSESANQAFLGTYVAPSVLDSIKGFSQFQPLASPRILNS 430
DB 356 FDEFTARTPTDSE--GVPRSANMHLFRGSSFVASSLIDQ-----EP---SQGLH-- 401
QY 431 PRVYVSP 438
DB 402 -KVFVHPI 408

```

RESULT 13  
US-10-369-493-5149  
Sequence 5149, Application US/10369493  
Publication No. US2003023675A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Yongwei  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.  
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
FILE REFERENCE: 38-10(52052)B  
CURRENT APPLICATION NUMBER: US/10/369,493  
CURRENT FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: US 60/360,039  
NUMBER OF SEQ ID NOS: 47374  
SEQ ID NO 5149  
LENGTH: 740  
TYPE: PRT  
ORGANISM: Caenorhabditis elegans  
US-10-369-493-5149

Query Match 36.4%; Score 951.5; DB 15; Length 740;  
Best Local Similarity 47.9%; Pred. No. 5,16-60;  
Matches 190; Conservative 69; Mismatches 105; Indels 33; Gaps 5;

```

QY 23 ETEEGSGEPELSPADACPLAELRAAGLEPVGHVEVELTETSVA--VGP-----BRIGP 77
DB 6 EYEFRAENIEEGGEKTDSS-----SETEIDIDGVAKCKEADP 44
QY 78 HCEPLRLVYKGGYGVQVQYKQVGTNIGKIYAMKYLAKKIVRNADOTAFNRARNTLE 137
DB 45 ROFELIKLVAGQSYGVFLVRKVGSDAQGLYAMKYLAKKATL--KVRDVRKX 102
QY 138 SVKGFPIYELAVAFQTKGLYLLIECLSGSELETHLEREGIFLEDYACFYLAETALGH 197
DB 103 HSHFFIYKLVHAFQTEGSKLYLLIDPLRGDLETRLSKEVMTSEOVKRYLAELH 162
QY 198 LHSQGIYIDKPEINMLSSQGHIXLTDGLCESEIHGAVHTTQCTEYVAPEILVRS 257
DB 163 LHSGLIYIDKPEINMLDADGHIXITDRLSGEALDHDRAVSFGTLEYNA 222
QY 256 GENRAVDWMSIGALMYDMLTGSPPPTAENRKKIMDKIRGKUALPPYLTPDARVKKFL 317
DB 223 GHSMAADPRLSLGAGIDGVEIRKHPPFTIDMTWTLRKIKPFPKAVGPRPDTH 282
QY 318 KNPSPQRIIGGSGDADVDQRHPPFRHMMDDLLAMVDPFRCLQSEEDVQ 377
DB 283 KNSQNRKLGAGIDGVEIRKHPPFTIDMTWTLRKIKPFPKAVGPRPDTH 342
QY 378 QTPVSDPTALSESAN--QAFVGYVAPSVLDSIK 412
DB 343 RPKDSP--ALPASANGHIFRGSFVSNVMEERK 376

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RESULT 14  
US-09-771-161A-265  
Sequence 265, Application US/09771161A  
Patent No. US20020110811A1  
GENERAL INFORMATION:  
APPLICANT: LEVINE, et al.  
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
FILE REFERENCE: 802620-2005.1  
CURRENT APPLICATION NUMBER: US/09/771,161A  
CURRENT FILING DATE: 2001-01-26  
PRIOR APPLICATION NUMBER: 09/724,676  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: 136776  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 135619  
PRIOR FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 273  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 265  
LENGTH: 740  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-771-161A-265

Query Match 36.3%; Score 949.5; DB 9; Length 740;  
 Best Local Similarity 48.7%; Pred. No. 7,1e-60;  
 Matches 185; Conservative 65; Mismatches 105; Indels 25; Gaps 4;

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QY 29 EGEPELSPADACIALRAAGLEPVGHTEVELTETS---VAVGERIGPHCELLR 84
DB 31 EPMGEERINP-----QTEBVSIKETAITHHVKEGHEKADPSQFELK 72
QY 85 VLGGGKGVQVRKVGQTNLGIYAMKYLKRAKIVRNADTAFTAEARNILLESVKHPFI 144
DB 73 VLGGGSPGVFLVKKISGSARQLYAMKYLKATL--KYRDRVTKMERDILVENVHPFI 130
QY 145 VELAYAFQTKGLYILIECLSGGELFTHLERBGFLBEDTACFYLAETTLAIGHLSGGII 204
DB 131 VKLHYAFQTEBKLYLIDFLRGGDLFTFLSKVETFEEDVGFYLAELALADHLSIGII 190
QY 205 YRDKPENIMLSGGHKLTDPLGCKESIHEGAVTHTECGTIEYMADEILVRSGNRAVD 264
DB 191 YRDKPENIILDEBGHKLTDPLGCKESIHEKKAIVSCGIVETMADEVVNRGHTQSAD 250
QY 265 WWSLGALMYDMLTGSPPPTAENRKKTMDKIIRGLALPYLTDPARDLVKKFLKRNPSOR 324
DB 251 WWSFGVLMFEMLTGTLFPGKDKRKETWTMLKALGMFQFLSPBAQSLRWLFKRNPNR 310
QY 325 IGGPGDAADVORHPFRHMMWDDLAMRVDPPEPRPCLOSEEDVSCDEFRTQTPTDPS 384
DB 311 LGAGPDGVEEIKKHSFSTIDMKLYRREIHPKPAATGRPEDTFFPDPEPTAKTPDPS 370
QY 385 DDTALSESANQAFLGFTYYA 404
DB 371 -GIPPSANAHQLFRGFSFYA 389

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## RESULT 15

US-09-771-161A-266  
 ; Sequence 266, Application US/09771161A  
 ; Patent No. US20020110811A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LEVIN, et al  
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
 ; FILE REFERENCE: 802620-2005.1  
 ; CURRENT APPLICATION NUMBER: US/09/771.161A  
 ; PRIOR FILING DATE: 2001-01-26  
 ; PRIOR APPLICATION NUMBER: 09/724,676  
 ; PRIOR FILING DATE: 2000-11-28  
 ; PRIOR APPLICATION NUMBER: 136776  
 ; PRIOR FILING DATE: 2000-06-15  
 ; PRIOR APPLICATION NUMBER: 135619  
 ; PRIOR FILING DATE: 2000-04-12  
 ; NUMBER OF SEQ ID NOS: 273  
 ; SOFTWARE: Patentia version 3.0  
 ; SEQ ID NO 266  
 ; LENGTH: 740  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-771-161A-266

Query Match 36.3%; Score 949.5; DB 9; Length 740;  
 Best Local Similarity 48.7%; Pred. No. 7,1e-60;  
 Matches 185; Conservative 65; Mismatches 105; Indels 25; Gaps 4;

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QY 29 EGEPELSPADACPLAEPLAAGLEPVGHTEVELTETS---VAVGERIGPHCELLR 84
DB 31 EPMGEERINP-----QTEBVSIXEIALTHHVKEGHEKADPSQFELK 72
QY 85 VLGGGKGVQVRKVGQTNLGIYAMKYLKRAKIVRNADTAFTAEARNILLESVKHPFI 144
DB 73 VLGGGSPGVFLVKKISGSARQLYAMKYLKATL--KYRDRVTKMERDILVENVHPFI 130
QY 145 VELAYAFQTKGLYILIECLSGGELFTHLERBGFLBEDTACFYLAETTLAIGHLSGGII 204
DB 131 VKLHYAFQTEBKLYLIDFLRGGDLFTFLSKVETFEEDVGFYLAELALADHLSIGII 190

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QY 205 YRDKPENIMLSGGHKLTDPLGCKESIHEGAVTHTECGTIEYMADEILVRSGNRAVD 264
DB 191 YRDKPENIILDEBGHKLTDPLGCKESIHEKKAIVSCGIVETMADEVVNRGHTQSAD 250
QY 265 WWSLGALMYDMLTGSPPPTAENRKKTMDKIIRGLALPYLTDPARDLVKKFLKRNPSOR 324
DB 251 WWSFGVLMFEMLTGTLFPGKDKRKETWTMLKALGMFQFLSPBAQSLRWLFKRNPNR 310
QY 325 IGGPGDAADVORHPFRHMMWDDLAMRVDPPEPRPCLOSEEDVSCDEFRTQTPTDPS 384
DB 311 LGAGPDGVEEIKKHSFSTIDMKLYRREIHPKPAATGRPEDTFFPDPEPTAKTPDPS 370
QY 385 DDTALSESANQAFLGFTYYA 404
DB 371 -GIPPSANAHQLFRGFSFYA 389

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Search completed: June 30, 2004, 17:20:18  
 Job time : 51 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 3, 2004, 12:01:17 / Search time 661 Seconds  
(without alignments)

3612.682 Million cell updates/sec

Title: US-09-762-258-2  
Sequence: 1 MARRRRRAGGAAAVFDL.....PIRPPGTTKKKXKRGRRGGR 495

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Delop 6.0, Delext 7.0

Searched: 3163042 seqs, 2412103600 residues

Total number of hits satisfying chosen parameters: 6326084

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-MAXLEN=200000000 -USER=US09762258 @cgn 1.1 487@rnatc.30062004.165610.13661  
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query SUMMARIES  
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2	1947.5	74.5	1637	10	US-09-968-433-10	Sequence 10, Appl
3	1748	66.9	2346	9	US-09-954-456-1137	Sequence 1137, Ap
4	1748	66.9	2346	10	US-09-920-677-3	Sequence 3, Appl
5	1748	66.9	2346	13	US-10-388-360-321	Sequence 321, Appl
6	1746	66.8	1800	15	US-10-316-253-31	Sequence 31, Appl
7	1740	66.6	2287	15	US-10-316-253-33	Sequence 33, Appl
8	1740	66.6	2287	16	US-10-191-803-230	Sequence 230, Appl
9	1724.5	66.0	2362	13	US-10-425-114-26874	Sequence 26874, A
10	1646	63.0	1197	13	US-09-925-298-245	Sequence 245, App
11	1646	63.0	1197	15	US-10-102-806-245	Sequence 245, App
12	1455	55.7	2556	9	US-09-817-310-1	Sequence 1, Appl
13	1406.5	53.8	1058	10	US-09-968-433-58	Sequence 58, Appl
14	1385.5	46.3	1607	16	US-10-305-720-146	Sequence 126, Appl
15	1211.5	46.3	843	13	US-10-220-955-1	Sequence 1, Appl
16	980.5	37.5	3206	16	US-10-159-553-155	Sequence 155, App
17	966	37.0	3061	9	US-09-880-107-2146	Sequence 2146, Ap
18	958	36.6	3673	15	US-10-240-965-1216	Sequence 1216, App
19	955.5	36.6	4098	16	US-10-108-260A-891	Sequence 891, App
20	942	36.0	669	16	US-10-305-720-118	Sequence 118, App
21	937.5	35.9	2403	15	US-10-102-554-1	Sequence 1, Appl
22	910.5	34.8	3169	13	US-10-425-114-26242	Sequence 26242, A
23	907.5	34.7	4563	14	US-10-002-600-14	Sequence 14, Appl
24	886.5	33.9	3131	13	US-10-342-887-972	Sequence 972, App
25	886.5	33.9	3131	13	US-10-172-118-972	Sequence 972, App
26	856	32.7	3120	15	US-10-112-286-1	Sequence 1, Appl
27	851.5	32.6	1666	13	US-10-424-559-34191	Sequence 34191, A
28	850.5	32.5	1440	13	US-10-425-114-7797	Sequence 7797, Ap
29	850	32.5	491	10	US-09-968-433-57	Sequence 57, Appl
30	844	32.3	594	13	US-10-240-315-2	Sequence 2, Appl
31	824	31.5	1335	16	US-10-116-275-285	Sequence 285, App
32	813.5	31.1	673	9	US-09-925-300-418	Sequence 418, App
33	810.5	31.0	1315	13	US-10-403-161-3	Sequence 3, Appl
34	810.5	31.0	1388	15	US-10-067-977-1	Sequence 1, Appl
35	810.5	31.0	2281	16	US-10-131-410-39	Sequence 39, Appl
36	810.5	31.0	2343	13	US-10-403-161-1	Sequence 1, Appl
37	810.5	31.0	2354	15	US-10-210-120-22	Sequence 22, Appl
38	810.5	31.0	2265	9	US-09-981-355-6	Sequence 6, Appl
39	810.5	31.0	3196	16	US-10-094-749-222	Sequence 222, Appl
40	807	30.9	2025	17	US-10-437-963-73382	Sequence 73382, A
41	806.5	30.9	2370	9	US-09-969-347-214	Sequence 214, App
42	806.5	30.9	2370	9	US-09-880-107-3855	Sequence 3855, Ap
43	806.5	30.9	2370	15	US-10-000-039-1	Sequence 1, Appl
44	806.5	30.9	2370	16	US-10-353-690-11	Sequence 11, Appl
45	804	30.8	1308	16	US-10-369-493-46340	Sequence 46340, A

## ALIGNMENTS

RESULT 1  
US-10-425-114-18480  
Sequence 18480, Application US/10425114  
Publication No. US2004003488BA1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jindong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E  
APPLICANT: Tabaka, Jack B  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 18480  
LENGTH: 1742  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Clone ID: LTB3081-101-B10\_FLI







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QY 1 MetAlaArgGlyAArgAlaArgGlyAlaGlyAlaAla----- 13
Db 28 ATAGAGCGAGAGAGAGAGCGGAGCGCTTTTACCCAGCCCCCGAGACTTCCGAGACAGGAA 87
QY 14 -----MetAlaAlaValPheAspLeuAspLeuGluThrGluGluGluSerGluGly 30
Db 88 GCTGAGGACATGGCAGAGAGGTGTTGACATGACCTGAGCCAGACAGAGCGGGGCTCT 147
QY 31 GluGlyGluProGluLeuSerProAlaAspAlaCysProLeuAlaGlu---LeuArgAla 49
Db 148 GAGGAGAGCTGAGG-----GAGGGGGGTCAGTTAAATGAAAGCATGAGCCAT 195
QY 50 AlaGlyLeuGluPro-----ValGlyHisThrGluGluGluAlaGluLeuThrGlu 65
Db 196 GGGGAGGTGAGCACAATGAGACTTGGCAGTGAACATTTGAGAAATTTGAAATCTCAGAA 255
QY 66 ThrSerValAsnValGlyProGluArgGlyGlyProHisCysPheGluLeuLeuAlaGly 85
Db 256 ACTAGTGTGAACAGAGGCGGAGAAATGACAGCAAGATGTTTGAAGCTACTTCCGGTA 315
QY 85 LeuGlyLeuGlyGlyGlyGlyValPheGluValArgGlyValGluGlyThrAsnLeu 105
Db 316 CTGGTAAAGGGGCTATGAGAAAGCTTTTCAAGTACGAAAGTAAAGAGAGCAATACT 375
QY 106 GlyLeuIleThrAlaMetLysValLeuArgGlyAlaLysIleValArgAsnAlaLysAsp 125
Db 376 GGGAAATATTTCCATGAAAGGTCTTAAAGGCAATGATGTAAGAAATGCTAAAGAT 435
QY 126 ThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIleVal 145
Db 436 ACAGCTCATACAAAGCAAGAGCAAGATTTCTGAGAGAGTAAAGATCCCTTCATCCTG 495
QY 146 GluLeuAlaIleThrAlaPheGlnThrGlyGlyLysLeuTyrosLeuGluCysLeuSer 165
Db 496 GATTATATTATTCCTTTCAGACTGGTGGAAACTTACCTCATCTTGAAGATCTCAGT 555
QY 166 GlyGlyGluLeuPheThrHisLeuGluArgGlyIlePheLeuGluAspThrAlaCys 185
Db 556 GAGAGGAACTATTATTCAGATTCAGAAAGAGGAGAAATTTATGAGAGACAGTGCCTGC 615
QY 186 PheTyrosLeuAlaGluIleThrLeuAlaLeuGlyHisLysHisSerGlnGlyIleIleTyr 205
Db 616 TTTTACTTGGCAGAAATCTCCAGTGGCTTTGGGCACTTTCATCAAAAGGGATCACTAC 675
QY 206 ArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLeuLeuThrAsp 225
Db 676 AGGAGCTTAAGCGGAGAAATATCATGCTTAATCACCAAGGTCATGTGAACCTAACAGAC 735
QY 226 PheGlyLeuCysLeuSerIleHisGluGlyAlaValThrHisThrPheCysGlyThr 245
Db 736 TTTGACTATGCAAAAGATCTATTCATGATGAGAACAGTCAACACACATTTGTGAGACA 795
QY 246 IleGluIleMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspThr 265
Db 796 ATAGAAATACATGCCCCCTGAAATCTTGATGAGAAAGGCGCAACATGTCGTGATGG 855
QY 266 TrpSerLeuGlyAlaLeuMetTyrosPheLeuThrGlySerProProPheThrAlaGlu 285
Db 856 TGGAGTTTGGAGCATTAATGATATGACATGCTGACGAGACACCCCATTCATCTGGAGAG 915
QY 286 AsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProProTyrosLeu 305
Db 916 AATAGAAAGAAACAAATGACAAATCTCAATGTAATCAATTTGCTCCCTAACCTC 975
QY 306 ThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArgIle 325
Db 976 ACACAGAGAGCCAGAGATCTGCTTAAGAGCTGCTGTAAGAAAGAAATCTCTGCTGCTG 1035
QY 326 GlyGlyGlyProGlyValAspAlaAlaAspValGlnArgHisProPhePheArgHisMetAsn 345
Db 1036 GAGAGCTGCTCGGGAGCCTGGAGAGTTCAGAGCTCATCCATCTTTTGAACATTAAC 1095
QY 346 TrpAspAspLeuLeuAlaTrpArgValAspProProPheArgProCysLeuGlnSerGlu 365

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Db 1096 TGGGAGAACTTCTGGCTCGAAGCTGAGAGCCCCCTTTAACTCTGTGTGATCTGA 1155
QY 366 GluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAsp 385
Db 1156 GAGAGTGAAGTCACTTGATTTCCAAAGTTTCACTCAGACACCTGTGACAGCCAGAT 1215
QY 386 AspThrAlaLeuSerGluSerAlaAsnGlnIlePheLeuGlyPheThrTyrosAlaPro 405
Db 1216 GACTCAACTCAGAGAAAGTCCCAATCAGGCTTTCTGGGTTTACATATGCTCCA 1275
QY 406 SerValLeuAspSerIleLysGlnGlyPheSerPheGlnProLysLeuArgSerProArg 425
Db 1276 TCTGTACTTGAAGAGTGAAGAAAGTTTCTTTGAAACCAAAATCGATCAGCTCA 1335
QY 426 ArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerPro-----Phe 443
Db 1336 AGATTTATTTGGAGCCACAGACACCTGTCAAGCCCAAGTCAATTTCTCTGGGATTTTC 1395
QY 444 GluGlyPheArgProSerProSerLeuProGluProThrGluLeuProLeuProLeu 463
Db 1396 TGGGAGAGAGGTCTTCGAGCAGC-----ACAGCAATCTCAGACACCTGTG 1443
QY 464 LeuProProProProProSer-----Thr 471
Db 1444 GAAATCCCAATGAGAAACAGTGGCATGAGACAGATGATGACAAATGATGGGAGAGCA 1503
QY 472 ThrAlaProLeuProIleArgProProSerGlyThrLys----- 484
Db 1504 TCGGACACACTTCCAAATCGACAGCCGAACTGGGCGCATACAAAAACAAGCTTTCCC 1563
QY 484 ----- 484
Db 1564 ATGATCTCCAAACGGCCAGAGCACCTGGGTATGAAATCTATGACAGAGCAATGCTTTAAT 1623
QY 485 -----LysSerLysArgGlyArgGlyArg 492
Db 1624 GAATTTAAGCAAAAGGTGAGAGAGGAGA 1653

RESULT 4
US-09-920-677-3
/ Sequence 3, Application US/09920677
/ Publication No. US2003083284A1
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ TITLE OF INVENTION: ANTISENSE MODULATION OF P70 S6 KINASE EXPRESSION
/ FILE REFERENCE: RTS-0245
/ CURRENT APPLICATION NUMBER: US/09/920,677
/ CURRENT FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 49
/ SEQ ID NO 3
/ LENGTH: 2346
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURES:
/ NAME/KEY: CDS
/ LOCATION: (28) ... (1605)
US-09-920-677-3

Alignment Scores:
Pred. No.: 1,04e-167 Length: 2346
Score: 1748.00 Matches: 354
Percent Similarity: 73.45% Conservative: 50
Best Local Similarity: 64.36% Mismatches: 80
Query Match: 66.87% Indels: 66
DB: 10 Gaps: 8

US-09-762-258-2 (1-495) x US-09-920-677-3 (1-2346)
QY 1 MetAlaArgGlyAArgAlaArgGlyAlaGlyAlaAla----- 13
Db 28 ATAGAGCGAGAGAGAGCGGAGCGCTTTTACCCAGCCCCCGAGACTTCCGAGACAGGAA 87

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QY 14 -----MetAlaValIlePheAspLeuAspLeuThrGluGluGlySerGluGly 30
Db GGTGAGACATGGCGAGTGTGTTGACATGACCTGACACCGACGAGGAGCTCT 147
QY 31 GluGlyGluProGluLeuSerProAlaAspAlaCysProLeuAlaGlu---LeuArgAla 49
Db GAGATGAGCTGGAG-----GAGGGGGCTCAGTTTAATGAAAGCCTGAGCAT 195
QY 50 AlaGlyLeuGluPro-----ValGlyHisTyrGluGluValGluGluLeuGlu 65
Db GGGGAGATTGACCATATGAACTTGGCATGAAACATTTGGAATTTGAAATCTCAGA 255
QY 66 ThrSerValAsnValGlyProGluArgGlyIleGlyProHisCysPheGluLeuLeuArgVal 85
Db ACTAGTGTGAACGAGGGCCGAGAAAAAATCAGACCAAGAAATTTTGGACTCTCTCGGGTA 315
QY 86 LeuGlyLeuGlyGlyTyrGlyValPheGluValAlaGlyValGluGlyValThrAsnLeu 105
Db CTGGTAAGGGGCGCTATGGAAGCTTTTCAAGTACGAAAGTAAGTACGAGCAAAATCT 375
QY 106 GlyValIleTyrAlaMetLeuValLeuArgGlyValAlaValArgAsnAlaLysAsp 125
Db GGGAAAAATTTGCTCAGTAAGTGTCTTAAAGGCAATGATGTAAGAAATGCTAAAGAT 435
QY 126 ThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIleVal 145
Db ACAAGCTATCAAAAGCGAAGCGAATTTCTGAGAGAAAGTAAGCAATCCCTTCACTG 495
QY 146 GluLeuAlaTyrAlaPheGluThrGlyGlyLysLeuTyrLeuIleLeuGluCysLeuSer 165
Db GATTAAATTTATGCTTTCAGACTGTGTGAAAACTCTACCTCATCTTGAATATCTCAGT 555
QY 166 GlyGlyGluLeuPheThrHisIleLeuGluArgGlyGlyIlePheLeuGluAspThrAlaCys 185
Db GAGGAGAACTATTATGCAAGTGAAGAGAGAGAAATATTATGAGAAAGACATGCTGCG 615
QY 186 PheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisIleHisSerGluGlyIleTyr 205
Db TTTTACTGGCAGAAATCTCATGCTTGGGCAATTACATCAAAAGGGGATCATCTAC 675
QY 206 ArgAspLeuLysProGluAsnIleMetLeuSerSerGluGlyHisIleLysLeuThrAsp 225
Db AGAAGCTGGAAGCGGAGAAATATCATGCTTAAACCAAGCTGTGGAACCTAAACGAC 735
QY 226 PheGlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThr 245
Db TTTGACCTATGCAAGATCTATTCATGATGGAACATGCAACACATTTTGTGAAACA 795
QY 246 IleGluTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyr 265
Db ATAAAGATACATGGCCCTGAAATCTTATGATGAGAGTGGCCCAATCTGCTGTGATGG 855
QY 266 ThrSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProPheThrAlaGlu 285
Db TGGAGTTTGGAGCATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 915
QY 286 AsnArgLysTyrThrMetAspLysIleIleArgGlyLysLeuAlaLeuProProTyrLeu 305
Db AATGAGAAAGAAAAAATGACAAATCTCTCAATGTAATCAATTTGCTCCCTACCTC 975
QY 306 ThrProAspAlaArgAspLeuValLysPheLeuLysArgAsnProSerGluAspGly 325
Db ACACAAAGAGCCAGAGATCTGCTTAAAGCTGTGAAAGAAATGCTGCTCTGCTGCTG 1035
QY 326 GlyGlyGlyProGlyAspAlaAlaAspValGluHisIleAspPhePheArgHisMetAsn 345
Db GGAAGCTGCTCTGGGAGAGCTGAGAGATTCAGAGCTCATCATCTTTAAGACATTAAC 1095
QY 346 ThrAspAspLeuLeuAlaTPrArgValAspProPheArgProCysLeuGluInserGlu 365
Db TGGAGAAATCTTCTGGCTGAGAGTGAAGCTCCCTTTAAACCTCTGTTGCAATCTGAA 1155

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QY 366 GluAspValSerGluPheAspThrArgPheThrArgGluInThrProValAspSerProAsp 385
Db GAGATGTAATCACTAGTTGATTTGATTCAGATTACAGTACAGACCTGTGACAGCCAGAT 1215
QY 386 AspThrAlaLeuSerGluSerIleAsnGluAlaPheLeuGlyPheThrTyrValAlaPro 405
Db GACTCAACTCTCAATGAAAGTGGCAATCAGGCTTTCTGGGTTTAAATATGTGGCTTCA 1275
QY 406 SerValLeuAspSerIleLysGluGlyPheSerPheGluInProLysLeuArgSerProArg 425
Db TCTGTACTTGAATGTGAAAGAAAGTTTCTTTTGAACCAAAATCCGATCACTGCA 1335
QY 426 ArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerPro-----Phe 443
Db AGATTATTTGGCAGCCCAAGCAACACCTGTGAGCCCAATCAAAATTTTCTCTGGGGAATTC 1395
QY 444 GluGlyPheArgProSerProSerProSerProGluProThrGluLeuProLeuProLeu 463
Db TGGGAAAGAGTGTCTTGGCCAGC-----ACAGCAATCTCTCAGACACTGTG 1443
QY 464 LeuProProProProProSer-----Thr 471
Db GAATACCCCAATGAAACAAAGTGCATAGACAGATGATGCAATGAGTGGGAAAGCA 1503
QY 472 ThrAlaProLeuProIleArgProProSerGlyThrLys----- 484
Db TGGCAGCACTTCCATATCAGACAGCCAGACTCTGGGCGATACAAAAACAAGCTTTCCC 1563
QY 484 ----- 484
Db ATGATCTCAAGCGGCGAGACACTGCTGATGATGATGATGATGATGATGATGATGAT 1623
QY 485 -----LysSerLysArgGlyArgGlyArg 492
Db GAATTTAAGGCAAAAGAGTGAAGAGGAGA 1653

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## RESULT 5

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US-10-388-360-321
; Sequence 321, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Jofire B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
; APPLICANT: Walker, Michael Graham
; TITLE OR INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; FILE REFERENCE: 39740-00010US
; CURRENT APPLICATION NUMBER: US/10/388,360
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-321
Alignment Scores:
Pred. No.: 1,046-167
Score: 1748.00
Percent Similarity: 73.45%
Best Local Similarity: 64.36%
Query Match: 66.87%
DB: 13
Gaps: 8
Length: 2346
Matches: 354
Conservative: 50
Mismatches: 80
Indels: 66

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US-09-762-258-2 (1-495) x US-10-388-360-321 (1-2346)



DB: 15 Gaps: 7

US-09-762-258-2 (1-495) x US-10-316-253-31 (1-1800)

QY 14 MetAlaValAlaPheAspLeuAspLeuThrGluGluGlySerGluGluGlyGlu 33

DB 134 ATGGAGGAGGTGTGGACATGACCTGGAGCCGACGAGATGAGGCTTGAAGATGAG 193

QY 34 ProGluSerProAlaAspAlaCysProLeuLagiU--LeuArgAlaAlaGlyLeu 52

DB 194 CTGGAG-----GAGGGGGGTGAGTTAAATGAAAGCAAGCAAGGAGGAGTT 241

QY 53 GluPro-----ValGlyHisTyrGluGluValGluLeuThrGluThrSerVal 68

DB 242 GGACCATATGAACTTGGCATGGAACATTTGTGAAATTTGAAATCTGAGAACTAGGTG 301

QY 69 AsnValGlyProGluArgIleGlyProHisCysPheGluLeuLeuAspValLeuGly 88

DB 302 AACAGAGGCGCAAAAATACGACCAATGTTTGGCTACTTGGGTACTTGGTAA 361

QY 89 GlyGlyTyrGlyValPheGluValArgGlyValGluGlyThrAsnLeuGlyVal 108

DB 362 GGGGGCTATGAAAGGTTTCAAGTACGAAAGTAAACAGAGCAAAATACGAGAAATA 421

QY 109 TyrAlaLeuValLeuArgValAlaValIleValArgAsnAlaAspThrAlaHis 128

DB 422 TTTCCTATGAGGTGCTTAAAGCAATGATGATGAAATGCTTAAAGATACAGCTCAT 481

QY 129 ThrArgAlaGluArgAsnIleLeuGluSerValIshHisProPheIleValGluLeu 148

DB 482 ACAAAACAGAGCGGAATATTCTGAGAGATGAAGCATCCCTTCATCGATTTATTT 541

QY 149 TyrAlaPheGluThrGlyGlyValLeuTyrLeuIleLeuGluCysLeuSerGlyGly 168

DB 542 TATGCTTTTACAGCCGGGAGAACTTACTCTTCACTTGAATCTCAGCTGAGAGAA 601

QY 169 LeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCysPheTyr 188

DB 602 CTATTATGACAGTTAGAAAGAGAGGGATTTTACAGAGATACAGCTTCTTTACTTG 661

QY 189 AlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGluGlyIleIleTyrArgAsp 208

DB 662 GCTGAATCTCCAGAGCTTTGGGGCATTTTCATTAATAAGAGATCTACAGAGACTG 721

QY 209 LysProGluAsnIleMetLeuSerSerGlyGlyHisIleLeuLeuThrAspPheGly 228

DB 722 AAGCCGAGAACATCACTTAAACACCAAGTCACTGAGAGCTTGAAGCTTGAAGCT 781

QY 229 CysIleGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIleGlu 248

DB 782 TGCAAAAGATCTATTCTGATGAGAACAGTCAAGCAATTTGTGAAACATATGATATC 841

QY 249 MetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspThrPheSer 268

DB 842 ATGCCCCCTGAATCTTGAATGAGAGAGCCCAACAGCTGTGAGATGAGTGGAGTTG 901

QY 269 GlyAlaLeuMetTyrAspMetLeuThrGlySerProPheThrAlaGluAsnArgGly 288

DB 902 GGAGCATTAATGATGATCATGCTGAGAGCACTTCATTCCTGGGAGGAAATAGAAAG 961

QY 289 LysThrMetAspIleIleLeuArgGlyValLeuAlaLeuProTyrLeuThrProAsp 308

DB 962 AAAACAAATTAACAAATCTCAATGTAATCTTAATTTGCTCCCTTACCTCAACAAG 1021

QY 309 AlaArgAspLeuValIshHisPheLeuValArgAsnProSerGluArgIleGlyGly 328

DB 1022 GCTCGAGATCTGCTTAAAGAGCTGCTGAAAGAAAGCTGCTCTGAGAGCTGAG 1081

QY 329 ProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetAsnThrPasp 348

DB 1082 CTGGGGATCTGGAGAGATCAAGCGCATCTTTTATGACACATTAATCTGGAGAGAG 1141

QY 349 LeuLeuAlaThrPargValAspProProPheArgProCysLeuGlnSerGluAlaVal 368

DB 1142 CTTTGCTCGAAGGTGAGAGCCCTTTAAGCTCTGTGCAATCTGAAGAGATGTG 1201

QY 369 SerGluPheAspThrArgPheThrArgGlnThrProValAspSerProAspAspThr 388

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QY 389 LeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyrValAlaProSerValLeu 408

DB 1262 CTCAGTAAAGTGCACCAACGAGCTTCTGCTGTTTATCATATATGCTTCATCTGTACTT 1321

QY 409 AspSerIleLeuGluGlyPheSerPheGlnProLysLeuArgSerProAlaGlyLeuAsn 428

DB 1322 GAAAGGTGAAAGAAAGTTTCTTTTGAACCAAAATCGATCGCTCGAAGATTTATTT 1381

QY 429 SerSerProArgValProValSerProLeuLysPheSerProPheGlu----- 444

DB 1382 GGTAGCCACGAAACGCTGTGACCCACGTAATTTCTTCTGGGATTTCTGGAGCA 1441

QY 445 GlyPheArgProSerProSerLeuProGlu--ProThrGluLeuProLeuProLeu 463

DB 1442 GGTGCTTACGCGACAGCAAGAAATCTTCAAGACACTGTGGAATACCAATGGAACAACT 1501

QY 464 LeuProProProProProSerThrThr-----AlaProLeuProIleArg 478

DB 1502 GGAATGAGACAGATGATGTGACACAGAGGGGAAAGCTTCAGGCGCACTTCATCCGA 1561

QY 479 ProPro--SerGlyThrIshSerLys 487

DB 1562 CAGCCCACTCTGGCCATCAAAAACAA 1591

RESULT 7

US-10-316-253-33

Sequence 33, Application US/10116253

Publication No. US20030162706A1

GENERAL INFORMATION:

APPLICANT: The Procter & Gamble Company

APPLICANT: Peters, Kevin

APPLICANT: Thompson, Larry

APPLICANT: Meng, Feng

APPLICANT: Greis, Kenneth

TITLE OF INVENTION: Angiogenesis Modulating Proteins

FILE REFERENCE: 8865M

CURRENT APPLICATION NUMBER: US/10/316,253

PRIOR FILING DATE: 2002-12-10

PRIOR APPLICATION NUMBER: US 60/355,295

PRIOR FILING DATE: 2002-02-08

NUMBER OF SEQ ID NOS: 308

SOFTWARE: PatentIn version 3.1

SEQ ID NO 33

LENGTH: 2287

TYPE: DNA

ORGANISM: Rattus norvegicus

FEATURE:

NAME/KEY: CDS

LOCATION: (22) .. (1599)

OTHER INFORMATION:

US-10-316-253-33

Alignment Scores:

Prod. No.: 6,54E-167 Length: 2287

Score: 1740.00 Matches: 349

Percent Similarity: 77.97% Conserved: 51

Best Local Similarity: 68.03% Mismatches: 83

Query Match: 66.56% Indels: 30

DB: 15 Gaps: 8

US-09-762-258-2 (1-495) x US-10-316-253-33 (1-2287)

QY 1 MetAlaArgGlyArgArgAlaArgGlyAlaGlyAlaIle----- 13

DB 22 ATGAGGCGACGACGAGAGGGGAGCGCTTTTACCAAGCGCTTACCTTCAGACAGAGGAA 81

QY	14	-----MetalalavalPheaspLeuaspLeuGlnthrcilGluGluSerGluGly	30
Db	82	GCGTAGGACATGCGCAGAGAGTGTTCATCATAGACTTGAGCCAGCCAGAGATGAGGCTCT	141
QY	31	GluGluGluProGluLeuSerProAlaSerAlaCysProLeuAlaGlu--LeuArgala	49
Db	142	GAGGATGACCTGGAG-----GAGGGGGGCTCAGTTAAATGAAGACAGCCAT	189
QY	50	AlaGluLeuGluPro-----ValGluHisThrGluGluAlaGluLeuThrGlu	65
Db	190	GGGGAGCTTGAGACCATATGAACTTGCGCATGGAAACATTTGAGAAATTTGAATCTGAA	249
QY	66	ThrSerValAsnValGlyProGluArgGluGluProHisCysPheGluLeuLeuArgVal	85
Db	250	ACTAGGTGAAACAGAGGGCCAGAAAATAATCAACCCAGAAATGTTTAGCTACTCGGTA	309
QY	86	LeuGluGlyGlyGlyTyrGluValPheGluValArgGlyValGluGlyThrAsnLeu	105
Db	310	CTTGTAAGAGGGGCTATGAAAGGTTTTTCAGATCGAAAGTAAACAGAGCAATTACT	369
QY	106	GlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAsp	125
Db	370	GGGAAGATTTTGCCCATGAGGCTTAAAGGSCATATGATAGAAATGCTAAAGAT	429
QY	126	ThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIleVal	145
Db	430	ACAGCTCATACAAAGACAGCGGATATTCGAGGAAGTAAAGCATCCCTTCATTTGG	489
QY	146	GluLeuAlaIleTyrAlaPheGluThrGlyLysLysTyrLeuIleLeuGluCysLeuSer	165
Db	490	CATTATATTAATGCTTTGACACCGGTGAAAACCTTACTCATCTTGAGTATTCAGT	549
QY	166	GlyGlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCys	185
Db	550	GGAGGAGAACTTTTATGACATTGAAAGAGGGGATATTATCATGGAATACAGCTTC	609
QY	186	PheTyrLeuAlaGluIlePheLeuAlaLeuGlyHisLeuHisSerGlnGlyIleLeuTyr	205
Db	610	TTTACTTGCGGAAATCCCATGCTTTGGGGCATTTACATCAAAAAGGGATATTCATAC	669
QY	206	ArgAspLeuLysProGluAsnIleMetLeuLeuSerSerGlnGlyHisIleLeuLysLeuThrAsp	225
Db	670	ACAGACCTGAGACCGGAGAACATCATGCTTATCATCCAAAGTCAAGTGAAGCTGACAGAC	729
QY	226	PheGlyLeuCysGlyGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThr	245
Db	730	TTTGACATATGCAAGAAATCTATTCATGATGGAACAGTCAACCAACATTTGTGGACA	789
QY	246	IleGluTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspThr	265
Db	790	ATGAAATACATGCGCCCTCGAATCTTGATGAGAAAGCGCCACAACCGTCTGTGATTCG	849
QY	266	TrpSerLeuGlyAlaLeuMetTyrArgPheMetLeuThrGlySerProProPheThrAlaGlu	285
Db	850	TGCACTCTGGGAGCATATATATATACATGCTGACGTGAGCACTTCATCTCGGGGAG	909
QY	286	AsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProProTyrLeu	305
Db	910	AATAGAAAGAAACAAATTCACAAATCCCTCAATGTAACTTAATTTGCTCTCCATCC	969
QY	306	ThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnAlaGle	325
Db	970	ACACAAAGAACTCGAGATCTGCTTAAAAAGCTGGAAGAAAGTGGCTTCGTGCTT	1022
QY	326	GlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetLeu	345
Db	1030	GGAGCTGGCCCTGGGAGATCTGGAAGAAGTCCAAAGCGCATCCATTTTATGACATCTAAC	1089
QY	346	TrpAspAspLeuLeuAlaIleTrpArgValAspProProPheArgProCysLeuGlnSerGlu	365
Db	1090	TGCGAAGAGCTTTTGGCTCGAAGGTGGAGGCCCTTTAAGCCTCTGTGTAATCTGAA	1144
QY	366	GluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAsp	385

Db	1150	GAGCATGTGAGTCAAGTTGATTTCAAAGTTTACTGTGACACCTCTTGAACGCCCCGAT	1209
Qy	386	AApThralaleuSerGluSerAlaSerGlnAlaPheIeuGlyPheThrTyValAlaPro	405
Db	1210	GACTCAACTCTCAGTGAAGGCCAACCAAGGCTCTTCTGGGCTTTTACATATGTGGCTCCA	1269
Qy	406	SeValIleuApsSerIleuGluGlyPheSerPheGlnProGlySleuArgSerProArg	425
Db	1270	TCTGACTTGAAGAGTGAAGAAAGAAAGTTTCTTTTGAACCAAAATCCGATCGCTCGA	1329
Qy	426	ArgIleuApsSerSerProArgValProValSerProIleuGlyPheSerProPheGlu---	444
Db	1330	AGATTATATGTGAGGCCACGAAGCGCTGTGACCCCAATATCTCTCTGGGGGATTC	1389
Qy	445	-----GlyPheArgProSerProSerIleuProGlu---ProThrGluIleuProIleu	460
Db	1390	TGGGACAGAGGCTTCAAGCCACGACCAAAATCTCTGACACACCTGTGAAATACCAATG	1449
Qy	461	ProProIleuProProProProProSerThrThr-----AlaProIleu	475
Db	1450	GAAACAAATGGAATAGACCAATGATGATGTACAAACGAGCGGAAAGCTTCAGCCCACTT	1509
Qy	476	ProIleArgProPro---SerGlyThrIleuSerIleuS 487	
Db	1510	CCAAATCCGACAGCCCACTCTGGGCGCATACAAAAACAA 1548	
RESULT 8			
	US-10-191-803-230		
	Sequence 230, Application US/10191803		
	Publication No. US20040014040A1		
	GENERAL INFORMATION:		
	APPLICANT: MENDRICK, Donna		
	APPLICANT: PORTER, Mark		
	APPLICANT: JOHNSON, Kory		
	APPLICANT: HIGGS, Brandon		
	APPLICANT: CASTLE, Arthur		
	APPLICANT: ELASHOFF, Michael		
	TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling		
	FILE REFERENCE: 44921-5090US		
	CURRENT APPLICATION NUMBER: US/10/191,803		
	CURRENT FILING DATE: 2002-07-10		
	PRIOR APPLICATION NUMBER: US 60/303,819		
	PRIOR FILING DATE: 2001-07-10		
	PRIOR APPLICATION NUMBER: US 60/305,623		
	PRIOR FILING DATE: 2001-07-17		
	PRIOR APPLICATION NUMBER: US 60/369,351		
	PRIOR FILING DATE: 2002-04-03		
	PRIOR APPLICATION NUMBER: US 60/377,611		
	PRIOR FILING DATE: 2002-05-06		
	NUMBER OF SEQ ID NOS: 1140		
	SOFTWARE: PatentIn Ver. 2.1		
	SEQ ID NO 230		
	LENGTH: 2287		
	TYPE: DNA		
	ORGANISM: Rattus norvegicus		
	FEATURE:		
	OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_031985		
	US-10-191-803-230		
Alignment Scores:			
	Pred. No.:	6,54e-167	2287
	Score:	1740.00	349
	Percent Similarity:	77.97%	Matches: 51
	Best Local Similarity:	68.03%	Mismatches: 83
	Query Match:	66.56%	Indels: 30
	DB:	16	Gaps: 8
US-09-762-258-2 (1-495) x US-10-191-803-230 (1-2287)			
Qy	1	MeclAlaArgGlyArgGArgAlaArgGlyAlaGlyAlaAla-----	13
Db	22	ATGAGGCGACGACGAGGAGCGGAGCGCTTTTATCCACGCGCTGACTTCGACACAGGGA 81	

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QY 14 -----MetAlaIaValPheAspLeuAspLeuThrGluGluGlySerGluGly 30
DB 82 GCTGAGACATGCGAGAGATGTTTATGACATGACCTGAGCCAGCCAGAGATGACAGGCTCT 141
QY 31 GluGluGluProGluLeuSerProAlaAspAlaCysProLeuAlaGlu---LeuArgAla 49
DB 142 GAGCATGACCTGAG-----GAGGGGGGTCTGATTAAATGAAAGCATGAGCAAT 189
QY 50 AlaGlyLeuGluPro-----ValGlyHisTyrGluGluValGluLeuThrGlu 65
DB 190 GGGGAGATTGACCATGATGAACTTGACGAACTTGAGAAATTTGAATCTCACAA 249
QY 66 ThrsValAspValGlyProGluArgGlyGlyProHisCysPheGluLeuLeuArgVal 85
DB 250 ACTAGTGTGACAGAGGGCCGAGAAAATCAGACCAAGATGTTTACCTCTCTGGGCTA 309
QY 86 LeuGlyGlyGlyGlyTyrGlyValPheGluValaGlyValaGluGlyThrAsnLeu 105
DB 310 CTGGTAAAGGGGGCTATGAAAGGTTTTCAGTACGAAAGTAAACAGAGCAAAATCT 369
QY 106 GlyValSerIleTyrAlaMetLeuValLeuArgGlyAlaValIleValArgAspAlaAsp 125
DB 370 GGAAGATATTGGCCATGATAGGTGCTTAAAGGCAATGATAGTAAAGTAAAGAT 429
QY 126 ThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValIysHisProPheIleVal 145
DB 430 ACAGCTCATCAAAAGCAAGCGAGGAAATTTCTGAGAGAGTAAAGCATCCCTTCAATTG 489
QY 146 GluLeuAlaIleTyrAlaPheGluThrGlyGlyLysLeuIleLeuGluCysLeuSer 165
DB 490 GATTAAATTATGCTCTTCAGACCGGTGAAAACTTACCCATCTTGAATCTAGT 549
QY 166 GlyGlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCys 185
DB 550 GAGAGAGACTATTATTCAGACTTGAAGAGAGGGGATATTCATGAGAGATACAGCTTC 609
QY 186 PheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGluGlyIleTyr 205
DB 610 TTTTACTGGCTGAAATCTCATGCTTGGGCACTTATCAATCAAAAGGATATCTAC 669
QY 206 ArgAspLeuLysProGluAsnIleMetLeuSerSerGluGlyIleLeuLeuThrAsp 225
DB 670 AGAGACCTGAAAGCGGAGAACATGCTTATATCAACCAAGCTCAGGAACTACAGAC 729
QY 226 PheGlyLeuCysLysGluSerIleHisGluGlyAlaValIleThrHisThrPheCysGlyThr 245
DB 730 TTTGACTATGCAAAAGATCTATTCAATGAGACAGTCAAGCAGCATTTTGTGAAACA 789
QY 246 IleGlyTyrMetAlaProGluIleLeuValArgSerGlyHisAspAlaGlyAlaAspTyr 265
DB 790 ATAGAATATGATGGCCCTGAAATCTTATGATGAAAGCGGCCCAACCGTCTGTGATATGG 849
QY 266 TrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThrAlaGlu 285
DB 850 TGGAGTCTGGAGACATTATATATGATGATGATGATGATGATGATGATGATGATGATGAT 909
QY 286 AsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProTyrLeu 305
DB 910 AATGAAAGAGACAAATGCAAAATCTCAAAATGTAATTAATTTGCTCCCTACCTC 969
QY 306 ThrProAspAlaArgAspLeuValLysPheLeuLysArgAsnProSerGluArgIle 325
DB 970 ACACAAAGAGCTCGAGATCTGCTTAAAGCTGCTGAAAGAAATGCTGCTCTCTGCTCT 1029
QY 326 GlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetAsn 345
DB 1030 GAGAGCTGGCCCTGGAGATGCTGAGAGATGCCAAGCGCATCATTTTAAACACATTAAC 1089
QY 346 TrpAspAspLeuLeuAlaTyrArgValAspProProPheArgProCysLeuGluSerGlu 365
DB 1090 TGGAGAGAGCTTTTGGCTCGAAGGTGAGAGCGCCCTTAAAGCTCTGTGTCATATCGAA 1149

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QY 366 GluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAsp 385
DB 1150 GAGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1209
QY 386 AspThrAlaLeuSerSerGluSerAlaAspAlaPheLeuGlyPheThrTyrValAlaPro 405
DB 1210 GACTCAACTCTCATGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1269
QY 406 SerValLeuAspSerIleLeuGlyGlyPheSerPheGluProLysLeuArgSerProArg 425
DB 1270 TCTGACTGTGAAGATGGAAGAAAGATTTTCTTTTGAACCAAAATCCGATCCCTCGA 1329
QY 426 ArgLeuAsnSerProArgValProValSerProLeuLysPheSerProPheGlu--- 444
DB 1330 AGATTATGTGTAGCCCAAGACCCCTGTGACCCCAAGATTCCTCTGGGGAATTC 1389
QY 445 -----GlyPheArgProSerProSerLeuProGlu---ProThrGluLeuProLeu 460
DB 1390 TGGGAGAGAGTGTCTCAGGACAGCAAAATCTCAGACACCTGTGGAATACCAATG 1449
QY 461 ProProLeuLeuProProProProProSerThrThr-----AlaProLeu 475
DB 1450 GAAACAGTGAATATGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1509
QY 476 ProLeuArgProPro---SerGlyThrLysLeuSerLys 487
DB 1510 CCATCCGACAGCCCAACTCTGGGCCCATACAAAGAAACAA 1548

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## RESULT 9

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US-10-425-114-26874
: Sequence 26874, Application US/10425114
: Publication No. US20040034888A1
: GENERAL INFORMATION:
: APPLICANT: Liu, Jingdong
: APPLICANT: Zhou, Yihua
: APPLICANT: Kovalic, David K.
: APPLICANT: Screen, Steven E.
: APPLICANT: Tabaska, Jack B.
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILER REFERENCE: 38-21(5313)B
: CURRENT APPLICATION NUMBER: US/10/425,114
: NUMBER OF SEQ ID NOS: 73128
: SEQ ID NO 26874
: LENGTH: 2362
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURES:
: OTHER INFORMATION: Clone ID: LIB4656-028-B10_FLI
US-10-425-114-26874

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## Alignment Scores:

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Pred. No.: 2,59e-165 Length: 2362
Score: 1724.50 Matches: 351
Percent Similarity: 73.80% Conservative: 49
Best Local Similarity: 64.76% Mismatches: 79
Query Match: 65,974 Indels: 63
DB: 13 Gaps: 9

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US-09-762-258-2 (1-495) x US-10-425-114-26874 (1-2362)

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QY 1 MetAlaArgGlyAlaArgAlaArgGlyAlaGlyAlaAla----- 13
DB 39 ATGAGGCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 98
QY 14 -----MetAlaIaValPheAspLeuAspLeuGluThrGluGluGlySerGluGly 30
DB 99 GCTGAGACATGCGAGATGTTTATGACATGACCTGAGCCAGCCAGAGAGAGAGAGAGAGAGAG 158
QY 31 GluGluGluProGluLeuSerProAlaAspAlaCysProLeuAlaGlu---LeuArgAla 49

```

Db 159 GAGATGAGCTGGAG-----GAGGGGGGTCACTTAATGAAGCATGACCAT 206  
 Qy 50 AAGlyLeuGIuPro-----ValGIHieTyrgIuGIuValGIuLeuThrgIu 65  
 Db 207 GGGGGAATGACCAATGAACTGGACGAACTTTGGAATAATTTGAAATCTAGAA 266  
 Qy 66 ThSerValasnaValGIProGIuArgIleGIProHieScySphGleuLeuArGVal 85  
 Db 267 ACTAGTGTGAACAGAGGGCCAGAAAAATCAGACCGAAGTCTTTGAGCTACTCCGGTA 326  
 Qy 86 LeuGIuLyseGIyGIyGIyValPheGIuValArgIyValGIuGIyThraLeu 105  
 Db 327 CTGGTAAGGGGCTATGAAAAGTTTTCAGATCGAAAGCTAACAGAGCAAACTACT 386  
 Qy 106 GIlyseIleTyraIleuValIleuArgValIleuValIleuValArgnaIleuAsp 125  
 Db 387 GGGAAATATTTGCCATGAGGTGCTTAAAGGCAATGATAGTAAATGCTAAAGAT 446  
 Qy 126 ThrAlaHisThrArgAlaGIuArgnaIleuGIuSerValIyshiSproPheIleVal 145  
 Db 447 ACAAGCTCATCAAAAGAGAAACGGAATATCTGAGAAAGTAAAGCATCCCTTCATGCTG 506  
 Qy 146 GIuLeuAlaTyraIleuGIuThrgIyGIyLyseLeuThrgIleuGIuCySleuSer 165  
 Db 507 GATTATATTATCTCTGAGCTGGGAAAACCTACTCACTTCACTGATCTCACT 566  
 Qy 166 GIyGIyGIuLeuPheThraIleuGIuArgIuGIyIlePheLeuGIuAspThraIle 184  
 Db 567 GAGAGAACTATTATGCAAGTTAGAAAGAGGAATATTATGAGAGCACTGCTGAG 626  
 Qy 184 ----- 184  
 Db 627 CTGAGTGAACGCTCTTCAACACAGTCTTCTTAACAGAACCATTCATCGGCTTT 686  
 Qy 185 -----CysPheTyraIleuAlaGIuIleThraIleuGIyshiSleuHisSer 200  
 Db 687 CTTCCTTGATTCCTTTACTTGGAGAAATCTCAATGCTTTGGGCAATTTACTCA 746  
 Qy 201 GIuGIyIleIleTyraArgAspleuLySproGIuAsnIleuLeuSerGIuGIyHis 220  
 Db 747 AAGGGGATCATCTACAGAGCTGAAAGCCGAGAAATATCATGCTATATACCAAGTCA 806  
 Qy 221 IleLyseLeuThraSphGlyLeuCySlyGIuSerIleHisGIuGIyAlaValThraHis 240  
 Db 807 GTGAACCTAACAGACTTTGACATGCAAGAAATCTTTCATGATGGAACAGCACAC 866  
 Qy 241 ThrPheCysGIyThraIleGIuTyraIleGIuIleValIleuValArgSerGIyHisAsn 260  
 Db 867 ACATTTTGTGAACAATAGATATCATGSCCTGGAATCTTGATGAGAGTGGCCACAT 926  
 Qy 261 ArgAlaValAspThraSphSerIleuGIyAlaLeuSerTyraSphLeuThrgIySerPro 280  
 Db 927 CGTGTGTGATTTGGAGTTGGAGCACTTATATATGACATGCTGATGAGACACC 986  
 Qy 281 ProPheThraIleGIuAsnArgIyLyshiThraSphLyIleIleArgIyLyseuAla 300  
 Db 987 CCATTCACCTGGAGATGAAAGAAACAATGACAAATCTCAAAATGTAACATCAT 1046  
 Qy 301 LeuProProTyraLeuThraSphAlaArgAspleuValIyLyshiSphLeuLySArgAsn 320  
 Db 1047 TTTCCTCCCTACTCTCAACAAGAGCCAGAGATCTCTTAAAGCTGCTGAAAGAAAT 1106  
 Qy 321 ProSerGIuArgIleGIyGIyGIyProGIyAspAlaAlaAspValGIuArgHisProPhe 340  
 Db 1107 GCTGCTTCCTGCTGGAGAGCTGCTCTGGGAGAGCTGAGAAAGTTCAAGCTATCATTC 1166  
 Qy 341 PheArgHisMetAsnThraSphAspleuLeuAlaIleArgValAspProPheArgPro 360  
 Db 1167 TTTAGACATTAACCTGGAAGAACTCTGCTGCAAGAGTGAAGCCCTCTTTAAACCT 1226  
 Qy 361 CyLeuGIuSerGIuGIuAspValIleGIuIlePheAspThraSphThraArgIuThrgPro 380  
 Db 1227 CTTTCAATCTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1286

Qy 381 ValAspSerProAspAspThraIleuSerGIuSerAlaAsnGIuAlaPheLeuGIyPhe 400  
 Db 1287 GTGACAGGCCAGAGACTCAACTCAGTGAAGTCCAAATCAGATGCTTTCTGGGTTT 1346  
 Qy 401 ThrTyraIleAlaProSerValIleuAspSerIleLyGIuGIyPheSerPheGIuProLyS 420  
 Db 1347 ACATATGTGCTCCCATCTGTACTTGAAGTGAAGAAAGTTTCTCTTGAACCAAA 1406  
 Qy 421 LeuArgSerProArgArgLeuAsnSerSerProArgValProValSerProLeuLySPh 440  
 Db 1407 ATCCCATCACTCGAAGATTATATGACGCCCAACAACCTGTGACGCCAGTCAATTT 1466  
 Qy 441 SerPro-----PheGIuGIyPheArgProSerProSerLeuProGIuProThrgIleu 458  
 Db 1467 TCTCTGGGATTTCTGGGAAAGAGCTCTTGCCACG-----ACAGCAAT 1514  
 Qy 459 ProLeuProProLeuProProProProSer----- 470  
 Db 1515 CCTCAGACACCTGTGGAATATCCCATATGAAAACAAGTGCATAGACAGATGATGTGACA 1574  
 Qy 471 -----ThrThraIleProLeuProIleArgProPro-----SerGIyThraLyS 485  
 Db 1575 ATGAGTGGGAGAGCATGCGCACACTTCATTAATGACAGCCGAATCTTGCGGCATACAA 1634  
 Qy 486 SerLyS 487  
 Db 1635 AAACAA 1640  
 RESULT 10  
 US-09-925-298-245  
 / Sequence 245, Application US/09925298  
 / Publication No. US20020039764A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Rosen et al.  
 / TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 / FILE REFERENCE: PA103  
 / CURRENT APPLICATION NUMBER: US/09/925,298  
 / PRIOR FILING DATE: 2001-08-10  
 / PRIOR APPLICATION NUMBER: PCT/US00/05861  
 / PRIOR FILING DATE: 2000-03-08  
 / PRIOR APPLICATION NUMBER: 60/124,270  
 / NUMBER OF SEQ ID NOS: 845  
 / SOFTWARE: ParentIn Ver. 2.0  
 / SEQ ID NO 245  
 / LENGTH: 1197  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / FEATURE:  
 / NAME/KEY: misc feature  
 / LOCATION: (218)  
 / OTHER INFORMATION: n equals a,t,g, or c  
 / NAME/KEY: misc feature  
 / LOCATION: (1197)  
 / OTHER INFORMATION: n equals a,t,g, or c  
 / US-09-925-298-245  
 Alignment Scores:  
 Pred. No.: 1,01e-157 Length: 1197  
 Score: 1646.00 Matches: 309  
 Percent Similarity: 98.72% Conservative: 0  
 Best Local Similarity: 98.72% Mismatches: 3  
 Query Match: 62.97% Indels: 1  
 Db: 13 Gaps: 0  
 US-09-762-258-2 (1-495) x US-09-925-298-245 (1-1197)  
 Qy 184 AlaCysPheTyraIleuAlaGIuIleThraIleuAlaLeuGIyshiSleuHisSerGIyIle 203  
 Db 13 GCTGCTTCTCACTGCTGAGATGATCAAGCTGCGCTGAGCCATCTCCACTCCAGGGCATC 72  
 Qy 204 IleTyraArgAspleuLySproGIuAsnIleuLeuSerGIuGIyHisIleLyseu 223



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Db      73  ATCTACCGGAGACCTCAAGCCCGAGAAACATGCTCAGACACCGGGCCACATAACTG 132
Qy      224  ThrAspPheGlyLeuCyLeuSerIleHisGlyAlaValThrHisPheCys 243
Db      133  ACCGACTTTRAGCTCTGCAAGAGCTCTATGAGGGCCGCTCCTACCTCACTTCTGC 192
Qy      244  GlyThrIleGlyTyrMetAlaPro-GluIleLeuValArgSerGlyHisAsnArgAlaVal 263
Db      193  GGCACCATTTGAGTACATGGCCCTGAGACATTTCTGGTGGCGAGTGGCCACAAACCGGGCTGT 252
Qy      263  AspTyrTrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProPhePheTh 283
Db      253  GGACTGGGAGAGCTCGGGGGCCCTGATGTACCACTGCTCCTGATGCGCCCTTTAC 312
Qy      283  ValGluAsnArgIleGlySerThrMetAspLeuIleIleArgIleGlyLeuAlaLeuProPr 303
Db      313  CGCAGAGAACCGGAGAAACCATGATGATGATCATCGGGGCAAGCTGGCACTGCCCCC 372
Qy      303  OTyrLeuThrProAspAlaArgAspLeuValIleValPheLeuHisArgAsnProSerGly 323
Db      373  CTACCTCAACCCCAAGATGCGGGAGCTGTGTAAGAGTTCTGAAACGGAAATCCACGCA 432
Qy      323  nArgIleGlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgH 343
Db      433  GCGGATTGGGGGTGGCCCAAGGGAGATGCTGCTGATGTGCAAGACATCCCTTTTCCGGCA 492
Qy      343  sMetAsnTrpAspAspLeuLeuAlaTrpArgValAspProProPheArgProCysLeuG 363
Db      493  CATAAATTTGGACACACTTCTGGGCTGCGCTGGTGGAGACCCCTTTCAGGGCCCTGTGCA 552
Qy      363  nSerGluGluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSe 383
Db      553  GTGAGAGAGAGACGTGAGCCAGTTTATACCCGCTTCAACGGCAGACGCGGTGGACAG 612
Qy      383  rProAspAspThrAlaLeuSerGlySerAlaAsnGlnAlaPheLeuGlyPheThrTyrVa 403
Db      613  TCCTGATGACACAGCCCTCAGCGAGACTGCCAACAGAGCCCTTCTGGGCTTCAATACGT 672
Qy      403  lAlaProSerValLeuAsnSerIleGlyGlyGlyPheSerPheGlnProIleuLeuArgSe 423
Db      673  GAGCCCTCTGTCTGTGACAGCATCAAGAGGCTTCTCTTCCAGCCCAAGCTGACCTC 732
Qy      423  rProArgArgLeuAsnSerSerProArgValProValSerProLeuGlyPheSerProP 443
Db      733  ACCAGAGCGCCTCAACAGTAGAGCCCGCGGGCCCGCTCAGGCCCTCAAGTTCTCCCTTT 792
Qy      443  eGluGlyPheArgProSerProSerLeuProGlnProThrGluLeuProIleuProIle 463
Db      793  TGAAGGGGTTCGGCCCAAGCCCAAGCTGCGAGAGCCCAAGAGCTACCTTACCTCCACT 852
Qy      463  uLeuProProProProSerThrThrAlaProLeuProIleArgProProSerGlyTh 483
Db      853  CTGGCAACCGGCGCGCCCTCGAACACCGGCCCTCTCCCATCGTCCCGCCCTCAAGGAGC 912
Qy      483  rLysLysSerLysArgGlyArgGlyArgProGlyArg 495
Db      913  CAAGAACTCCAAAGAGGGGCGTGGCGCTCCAGGGGCGC 949

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## RESULT 11

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US-10-102-806-245
: Sequence 245, Application US/10102806
: Publication No. US20030054421A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: P4103P1C1
: CURRENT APPLICATION NUMBER: US/10/102,806
: PRIOR FILING DATE: 2002-03-22
: PRIOR APPLICATION NUMBER: 09/925,298
: PRIOR FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05881
: PRIOR FILING DATE: 2000-03-08

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: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 846
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 245
: LENGTH: 1197
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (218)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc feature
: LOCATION: (1193)
: OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-245

Alignment Scores:
Pred. No.: 1,01e-157 Length: 1197
Score: 1646.00 Matches: 309
Percent Similarity: 98.72% Conservative: 0
Best Local Similarity: 98.72% Mismatches: 3
Query Match: 62.97% Indels: 1
DB: 15 Gaps: 0

US-09-762-258-2 (1-495) x US-10-102-806-245 (1-1197)

Qy      184  AlaCyPheThrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIle 203
Db      13  GCTGCTTCTACCTGCTGCTGATCAAGCTGGCCCTTGGGCACTCTCAGCTCCAGGGCATC 72
Qy      204  lIeTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeu 223
Db      73  ATTACCGGAGACTTCAAGCTCCAGAACATCATCTCAGAACCGAGGGCCACATCAACTG 132
Qy      224  ThrAspPheGlyLeuCyLeuSerIleHisGlyAlaValThrHisPheCys 243
Db      133  ACCGACTTTRAGCTCTGCAAGAGCTCTATGAGGGCCGCTCCTACCTCACTTCTGC 192
Qy      244  GlyThrIleGlyTyrMetAlaPro-GluIleLeuValArgSerGlyHisAsnArgAlaVal 263
Db      193  GGCACCATTTGAGTACATGGCCCTGAGACATGTGATGAGGAGCTGCGCAACCGGGCTGT 252
Qy      263  AspTyrTrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProPhePheTh 283
Db      253  GGACTGGGAGAGCTCGGGGGCCCTGATGTACAGACATGCTCAGATGCGCCCTTTAC 312
Qy      283  ValGluAsnArgIleGlySerThrMetAspLeuIleIleArgIleGlyLeuAlaLeuProPr 303
Db      313  CGCAGAGAACCGGAGAAACCATGATGATGATCATCGGGGCAAGCTGGCACTGCCCCC 372
Qy      303  OTyrLeuThrProAspAlaArgAspLeuValIleValPheLeuHisArgAsnProSerGly 323
Db      373  CTACCTCAACCCCAAGATGCGGGAGCTGTGTAAGAGTTCTGAAACGGAAATCCACGCA 432
Qy      323  nArgIleGlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgH 343
Db      433  GCGGATTGGGGGTGGCCCAAGGGAGATGCTGCTGATGTGCAAGACATCCCTTTTCCGGCA 492
Qy      343  sMetAsnTrpAspAspLeuLeuAlaTrpArgValAspProProPheArgProCysLeuG 363
Db      493  CATGAATTTGGACACACTTCTGGGCTGCGCTGGTGGAGACCCCTTTCAGGGCCCTGTGCA 552
Qy      363  nSerGluGluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSe 383
Db      553  GTCAAGAGAGAGAGCTGAGGCAAGTTGATACCGCTTCAACAGGCAAGCGCGGTGACAG 612
Qy      383  rProAspAspThrAlaLeuSerGlnPheAsnGlnAlaPheLeuGlyPheThrTyrVa 403
Db      613  TCCTGATGACACAGCCCTCAGAGAGATGCGCAAGAGCTTCTCGGCTTCACTACT 672
Qy      403  lAlaProSerValLeuAspSerIleGlyGlyGlyPheSerPheGlnProIleuLeuArgSe 423

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OY	121	ArgSnaIaIaYsApRThraIahisIThRgAlaGluRgRgSniIleuGInuSerValIys	140
Db	825	ACCAATCAAAAGGACACAGCGCACCCGGGCCAGGCGCAATTAATCTGAGGCGTCAAG	884
OY	141	HisProHeIleValGluLeuAlaTYrAlaPheGInThRgIyIySleuTYrLeuIle	160
Db	885	CATCCCTTCAATAGTGAAGTAGTTATAGCTTCACAGACAGGAAAACATATACCTATA	944
OY	161	LeuGluCYsleuSerGlyIyGluLeuPheThRHisIleuGluIaRgGluGlyIlePheIeu	180
Db	945	CTTGAATAATCTCACCGGTTGAGAGACTTGTATGCAATTTGAGCTGAGGCGATCTTTTA	1004
OY	181	GluAspThraIaCYsPheTYrLeuAlaGluIleThRleuAlaLeuGlyHisIleuHisSer	200
Db	1005	GAGGATACCAATCCTCTCTATCTRAAGGAATCATTTTGCTTGGCCCTTGCACATACAA	1064
OY	201	GInGlyIleIleIyTYrAqAspLeuIyAspProGluSniIleuLeuSerGInGlyHis	220
Db	1065	CTGGGCAATCATCTCCCGCATCTGAAACCCGAGAACTACTGCTCGATGCAAGGACAT	1124
OY	221	IleIySleuThraPhePheGlyLeuCYsIleGluSerIleHisGluGlyAlaValThRHis	240
Db	1125	GTGAAGCTCCAGACCTTGAAGCTTGCAGAGACACATCAAGAGGATATTGTCAACCAC	1184
OY	241	ThRPhcCYsGlyThRleGluIyTYrMeAlaProGluIleLeuValArgSerGlyHisAsn	260
Db	1185	ACCTTTCGCGGCACAATTTAGTACATGAGCACTGAATTTTGACCAAGTGGCCATAGC	1244
OY	261	ArgAlaValAspTYrPTrpSerLeuGlyAlaIleuMeCYrAspMeLeuThnGlySerPro	280
Db	1245	AAACACAGTCACATGTAATCTCGGGGCGCTTCATGTTGACATGCTTCAAGAGTCCCA	1304
OY	281	ProPheThraIaGluAsnArgIySlyIyThMeAspIySleIleArgGlyIySleuAla	300
Db	1305	CCCTTACCGCGGAGATCCGAGAAGACATCAAGACATCTGAAAGCCAACTCAT	1364
OY	301	LeuProProTYrLeuThraProAspAlaArgAspLeuValIySlySPhleuIyArgAsn	320
Db	1365	CTGCACGCTTAACCTCACACCGAAGCCAGGAGATGTGTGCTGCCCTGATTAACCGGAG	1424
OY	321	ProSerGlnArgIleGlyGlyIyProGlyAspAlaIaAspValGInArgHisProPhe	340
Db	1425	GAACTCAAGCCCTTGGCAAGCGACCCGAGAGATCCGGCGCTTCAAAATACCCATTC	1484
OY	341	PheArgHisMeIaSnITPAspAspLeuLeuAlaTYrArgValaAspProProPheArgPro	360
Db	1485	TTCAAAACACGTCACCTGGAGCGATGTCTCCCGACAGCGCTCGCGCCCTATTAACCG	1544
OY	361	CysIeuGInuSerGluGluAspValSerGluPheAspThraArgPheThraArgGluThRPro	380
Db	1545	CTCTTGAGAAACCGAGAGATGATGTCTCAAGTTCATACAGATTCAAGACGAAATTCCA	1604
OY	381	ValAspSerProAspAspThraIaLeuSerGluSerIaIaSngInAlaPheLeuGlyPhe	400
Db	1605	GTGATTCGCCCTGATGATACAAACCTAAGCAAGTGCATTAATTTTCAAGGTTTC	1664
OY	401	ThTYrValAlaProSerValLeuAspSerIleIySgluGlyPheSerPheGluProIyS	420
Db	1665	ACCAACGTTGACACCTCGATACCTAGAGAGATATGCAATGG-----GCCAACCGAGTCCA	1718
OY	421	LeuArgSerProArgArg-LeuAsnSerSerProArgValProValSer-----	436
Db	1719	GCAGGCTCCCAAGACGATCTCCACGCGAGCTGCCGACACAGCTTCCGCTCGCATGTC	1778
OY	437	-----ProIeuIySPhneSerProPheGluGlyPhe-----	446
Db	1779	CCATCGGCAATGTCGCGGCCAAAGCCGCTGCGCATGCACGCTCATTTGCGACGATC	1838
OY	447	-----ArgProSe-----	449
Db	1839	CGGATGTTTGCACAGACCAACCGCCGCGCATCATGCACAGCATTTTGCGCGGCTCATC	1898

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Qy 449 rProSeuProGluProThrGlu-----LeuPro-----LeuProPr 462
Db 1999 GCCGCGGAGAGACGATGATGACGTCAGGGCTGCGGATGCTTAAAGCTGAGCG 1958
Qy 462 oLeuLeuProProProProProSerThrThraLeProLeuProLeaPro----- 479
Db 1959 ATTGCTTCCCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 2018
Qy 480 -----ProSeuGlyThrLysLysSerLysArgLysArgLysArg 492
Db 2019 CATCAATAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2078
Qy 492 G 492
Db 2079 A 2079

RESULT 13
US-09-968-433-58
; Sequence 58, Application US/09968433
; Publication No. US20030073162A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murthy, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PC-0051 CIP
; CURRENT APPLICATION NUMBER: US/09/968,433
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PERL Program
; SEQ ID NO: 58
; LENGTH: 1058
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030073162A1 037196_Mm.1
US-09-968-433-58

Alignment Scores:
Pred. No.: 2,1e-133 Length: 1058
Score: 1406.50 Matches: 280
Percent Similarity: 85.21% Conservative: 8
Best Local Similarity: 82.84% Mismatches: 12
Query Match: 53.81% Indels: 39
DB: Gaps: 1

US-09-762-258-2 (1-495) x US-09-968-433-58 (1-1058)
Qy 4 G1YArgArgAlaArgGlyAlaGlyAlaAlaMetAlaAlaValPheAspLeuAspLeuGlu 23
Db 48 GGCCAGAGGTCCTCCCGGAGCCGGGGGGCCATGCGCCGCTATTTAGTTAGCTTGAG 107
Qy 24 ThrGluGluGlySerGluGlyGlyGlyGluProGluLeuSerProAlaAspAlaCysPro 43
Db 108 ACCGAGGAGAGGAGCGAGCGGCGGCGGAGCGGAGCTTCGCGCTCGGAGCGTGTCTCC 167
Qy 44 LeuAlaGluLeuArgAlaAlaGlyLeuGluProValGlyHisGlyGluGluValGluLeu 63
Db 168 CTTGGCGAATTAAAGGCTGCTGCGCTGAGACAGTGGGACATATGAGAGAGTAGACTG 227
Qy 64 ThrGluThrSerValaAsnValaGlyProGluArgIleGlyProHisCysPheGluLeu 83
Db 228 ACAGAGAGGAGCGCTGAACCTGGGTCTGAGCGCATCGGCGCCACTGCTTGAAGTACTG 287
Qy 84 ArgValLeuGluGlySerGlyGlyGlyGlyValPheGluValaProGlyValaGluGlyThr 103
Db 288 AGTGTACTGGGCAAGGGGGGCTATGAGAGGTTCTCCAGGTGAGAAAGTGCAAGGACC 347
Qy 104 AsnLeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValaArgAsnAla 123

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Db 348 AACTGGGAAAAAATATATGCCATGAGAGTCTTAAGAGGCCAAGATTGATGACGTGCC 407
Qy 124 LysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPhe 143
Db 408 AAGGACAGACCCCATACCCCGGCTGAGAGGAGACATTTATTAATCTGTGAAGCATCTTCC 467
Qy 144 IleValGluLeuAlaTyrAlaPheGluThrGlyGlyLysLeuTyrLeuIleLeuGluCys 163
Db 468 ATTGTGAACTGGCTTATGCTTTCAGACAGGTGGGAAACTTACCTCATCTCGAGGTGC 527
Qy 164 LeuSerGlyValGluLeuPheThrHisIleGluArgGluGlyIlePheLeuGluAspThr 183
Db 528 CTAGTGTGTGTAGCTCTTCAACATCTTGAAGGAGAGGAGGAGGAGGAGGAGGAGGAGG 587
Qy 184 AlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGluGlyIle 203
Db 588 GCCTGCTTCACTGGCAGAGATCACATGAGCCCTGGGCGCATCTCCATCTCCCGC 646
Qy 204 IleTyrArgAspLeuSerProGluAsnIleMetLeuSerSerGluGlyHisIleLysLeu 223
Db 647 ATCTACCGGAGCTCAAGCCTGAGACATCATATCTGAGAGCGGAGGAGGAGGAGGAGGAG 706
Qy 224 ThrAspPheGlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCys 243
Db 707 ACAGACTTGGACTTGGCAAGAGGTCATTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 766
Qy 244 GlyThrIleGluTyrMetAlaProGluIleLeuValaArgSerGlyHisAsnArgAlaVal 263
Db 767 GGCACCATTTGAGTACATGAGCCCGGAGATTTCTAGGCGGAGGAGGAGGAGGAGGAGGAG 826
Qy 263 LAspTyrPheSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySer----- 279
Db 827 GACCTGTGAGCTGGAGGAGCCTGATGTACATGATGCTCAGTGGCAGATGCCAGC 886
Qy 279 ----- 279
Db 887 TTCCTGGCGAGGAGGTGTGTGAGGAGATCCCTTCCAGATTGGGCGAGAGTGGGTG 946
Qy 280 -----ProProPheThrAlaGluAs 286
Db 947 GAGAGACCCCTAGGCTGCGCTCACTTCTGCTTCCAGCGCCCTTCACTGCAAGAGAA 1006
Qy 286 nArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProPro 303
Db 1007 CCGAAGAAATCATGATTAATCATTAAGGAGAGCTGCTGCTGACACCC 1058

RESULT 14
US-10-305-720-126
; Sequence 126, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Express
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO: 126
; LENGTH: 1607
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040010136A1 1309709
; NAME/KEY: unsure
; LOCATION: (1) ... (1607)
; OTHER INFORMATION: a, t, c, g, or other
US-10-305-720-126

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## Alignment Scores:

Pred. No.:	5,13e-131	Length:	1607
Score:	1385.50	Matches:	285
Percent Similarity:	70.65%	Conservative:	40
Best Local Similarity:	61.96%	Mismatches:	69
Query Match:	53.00%	Indels:	67
		Gaps:	10

US-09-762-258-2 (1-495) x US-10-305-720-126 (1-1607)

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Qy      86 LeuGlyysGlyGlyGlyValPheGlnValArgValGlnGlyThrAsnLeu 105
Db      227 CTGGGGAGGCGCTCATGCCAGTGCAGACCTGC-----ATTACCTG 271
Qy      106 -----GlyValIleValMetLysValLeuArg-----LysAla 117
Db      272 ATCACCGACGAGAGTACCCGTCANATCATGTTTTTTTCAGGCGCACATTCCGAGC 331
Qy      118 LysIleValArgAlaLysAspThrAlaHisThrArgAlaGluArgAlaIleLeuGlu 137
Db      332 AGGGTTTCAGGAGGTGAGATGCTGTACCGAGTCCAGGAGACAGAAAGCTCTAGAG 391
Qy      138 SerValLysHisProPheIleValGluLeuAlaTyrAlaPheGlnThrGlyLysLeu 157
Db      392 CTGATTGAGTTC-----TTCCAGAGAGAGAGACCCCTTC 424
Qy      158 TyrIleuIleuGluCysLeuSerGlyGlyGluLeuPheThrHisLeuGluArgGluGly 177
Db      425 TACCTGGTGTGTTGAGAGATGCGGGGAGGCTCCATCTCTGAGCCACATCCACAAAGCCGCG 484
Qy      178 IlePheLeuGluAspThrAlaCysPheTyrIleuAlaGluIleThrIleuAlaLeuGlyHis 197
Db      485 CACTTCACAGAGCTGAGAGCCAGGCTGTGTGTGAGAGACGTGCCAGCGCTTGAGACTT 544
Qy      198 LeuHisSerGlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSerSer 217
Db      545 CTCGATTAACAAGAGCATGCCCCACAGAGACCTTAAGCCGGAACATCTCTGTGAGCAC 604
Qy      218 GlnGlyHis-----IleLysLeuThrAspPheGlyLeu----- 228
Db      605 CCCAACAGAGTCTCCCGCGTGAATCTGTGACTTCACCTGAGCGAGCGGCATCAAACTC 664
Qy      229 -----CysLysGluSerIleHisGluGlyAla-ValThrHisThrPheCysGlyTh 245
Db      665 AACGGGAGTGTCTCCCTAT-CTCCACCCCGAGAGCTCTCACTCCG-----TGCGGCTC 717
Qy      245 rIleGluTyrMetAlaProGluIle----- 253
Db      718 GCGGAGTACATGCGCCCGAGAGTGTGAGAGCTTCAGCGAGAGCTACATTCACGA 777
Qy      254 -----LeuValArgSerGlyHisAs 260
Db      778 CAAGCGCTGCGACCTGTGAGAGCTGCGGCTCATCTTATATCTACTACGCGGCTTACC 837
Qy      260 naGAlaValAsp---TTPTrSer-----LeuGlyAlaLeuMetTyrAspMetIle 276
Db      838 GCCCTTGCTGGCGCGCTGTGTGAGAGCGACTGCGGCTGAGACCGCTATGTACACATGCT 897
Qy      276 uThrGlySerProPheThrAlaGluAsnArgLysLysThrMetAspLysIleLeu 296
Db      898 CACTGGAATCCCGCCCTTTACCGGAGAAACCGGAAGAAACATGATAGATCATCCAG 957
Qy      296 gGlyLysLeuAlaLeuProPheTyrLeuThrProAspAlaArgAspLeuValLysLys 316
Db      958 GGGGAGAGCTGCGACTTCCCTACCTACCCAGAGAGCCCGGAGACCTTGTCAAAAGTT 1017
Qy      316 eleuLysArgAsnProSerGlnArgIleGlyGlyLysProGlyAspAlaAlaAspValG 336
Db      1018 TCTGAACGGAATCCAGCCAGAGATGGGGGTGGCCCGAGGATCTCTCTATGTCA 1077
Qy      336 naGHisProPheThrArgHisMetAsnTyrAspAspLeuLeuAlaTyrArgValAspPr 356
Db      1078 GAGAGATCCCTTTTTCGGGACATGATGTGAGAGACCTTCTGCGCTGGGTGTGAGACC 1137

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Qy      356 oProPheArgProCysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPheTh 376
Db      1138 CCGTTTCAGGCGCTGTCTGTCACTCAGAGAGAGACGTGACCGCATTTGATACCCGCTTCC 1197
Qy      376 rArgGlnThrProValAspSerProAspAspThrAlaLeuSerGluSerAlaAsnGlnAl 396
Db      1198 ACGGACAGAGCGCGGTGACATGCTGTATGACACAGCCCTCAGAGAGTGCACACAGGCG 1257
Qy      396 aPheLeuGlyPheThrTyrValAlaProSerValLeuAspSerIleLysGluGlyPheSe 416
Db      1258 CTTCCTGAGCTTACATACCTGAGCGCGCTGTCTCTGACAGACATTAAGAGGCTTCTC 1317
Qy      416 rPheGlnProLysLeuArgSerProArgArgLeuAsnSerSerProArgValProValSe 436
Db      1318 CTTCGAGCCCAAGCTGCGCTCACCGAGCGCTCAACATGATACCCCGGCTCCCTCTCCG 1377
Qy      436 rProLeuLysPheSerProPheGluGlyPheArgProSerProSerLeuProGluProTh 456
Db      1378 CCGCTCAAGTCTCTCCCTTTGAGGGGTTTGCGCCAGCCCGAGCTTCGCGAGCCGAC 1437
Qy      456 rGluLeuProLeuProProLeuLeuProProProProSerThrAlaProLeuPr 476
Db      1438 GGAGCTACCTTACCTCCACTCTCGACCGCGCGCGCTCGACCAACCGCCCTCTCC 1497
Qy      476 oIleArgProProSerGlyThrLysSerLysArgGlyArgGlyArgProGlyArg 495
Db      1498 CATTGCTCCCTCCCTCAGGACCAAGAGTCCAAAGAGGGGCGGTGGCGTCAAGGGCGT 1555

RESULT 15
US-10-220-955-1
? Sequence 1: Application US/10220955
? Publication No. US20030211989A1
? GENERAL INFORMATION:
? APPLICANT: PLOMMAN, GREGORY D.
? APPLICANT: WHITE, DAVID
? APPLICANT: MANNING, GERARD
? APPLICANT: SUDARSANAM, SUCHA
? APPLICANT: MARTINEZ, RICARDO
? TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
? TITLE OF INVENTION: ENZYMES
? FILE REFERENCE: 038602-1401
? CURRENT APPLICATION NUMBER: US/10/220,955
? CURRENT FILING DATE: 2001-03-02
? NUMBER OF SEQ ID NOS: 40
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 1
? LENGTH: 843
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-10-220-955-1

Alignment Scores:
Pred. No.: 1,12e-113
Score: 1211.50
Percent Similarity: 90.07%
Best Local Similarity: 79.43%
Query Match: 46.35%
DB: 13 Gaps: 1

US-09-762-258-2 (1-495) x US-10-220-955-1 (1-843)
Qy      117 AlaLysIleValArgAspAlaLysAspThrAlaHisThrArgAlaGluArgAsnIleLeu 136
Db      1 GGAATGAATGTAAGAAATGCTAAAGATACAGCTCATACAAAGACAGAAATGAAATTTCTG 60
Qy      137 GluSerValLysHisProPheIleValGluLeuAlaTyrAlaPheGlnThrGlyLys 156
Db      61 GAGGAAGTAGAGCATCCCTTATCTGTGATTTAATGCTTCAAGCTGTGAGAAAA 120
Qy      157 LeuTyrIleuIleuGluCysLeuSerGlyGlyGluLeuPheThrHisIleuGluArgGlu 176
Db      121 CTCTACTCATCTCTTGAATCTCAGTGAAGAGAACTATTTATGCAATTAGAAAGAGAG 180

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QY 177 GlyIlePheLeuGluAspThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGly 196
DB 181 GGAATATTATTATGAGAGACTGCTGCTTTACTTGCGAGAAATCTCCATGCGCTTGGGA 240
QY 197 HisLeuHisSerGlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSer 216
DB 241 CATTACATCAAAAGGGGATCATATACAGAGACTGAAAGCCGAGAAATATCATCTTAAAT 300
QY 217 SerGlnGlyHisIleLeuLeuThrAspPheGlyLeuCysLysGluSerIleHisGluGly 236
DB 301 CACCAAGGTCATATGAAATCAACAGACTTGGACTACGGAAGAAATCATATCATATGGA 360
QY 237 AlaValThrHisThrPheCysGlyThrIleGluTyrMetAlaProGluIleLeuValArg 256
DB 361 ACAGTCACACACACATTTTGTGGAACAATAGATACATGCCCCCTGAATCTTGATGAGA 420
QY 257 SerGlyHisAsnArgAlaValAspThrPheSerLeuGluAlaLeuMetTyrAspMetLeu 276
DB 421 AATGCGCACATCGTGTGTGAGTGTGAGATTTGGAGCATTAATGATGACATGCTG 480
QY 277 ThrGlySerProPheThrAlaGluAsnArgLysLysThrMetAspLysIleIleArg 296
DB 481 ACTGAGACACCCCCCATTTACTGCGGAGATAGAGAAAGAAACAATGACACATCCTCAA 540
QY 297 GlyValLeuAlaLeuProProTyrIleThrProAspAlaArgAspLeuValLysPhe 316
DB 541 TGTAACTCAATTGTGCTCTTACTCTCACACAAAGCCAGAGATCTGTTAAAGGCTG 600
QY 317 LeuLysArgAsnProSerGlnArgIleGlyGlyProGlyAspAlaAlaAspValGln 336
DB 601 CTGAAAGAAAGATGCTTCTCT--CTGGAGCTGTCTCTGGGACGCTGAGAAATTCA 657
QY 337 ArgHisProPhePheArgHisMetAsnTrpAspAspLeuAlaTrpArgValAspPro 356
DB 658 GCTCATTCATCTTTAGACACATTAAGTGGAGAACTTCTGGCTCAAAAGGTGAGGCC 717
QY 357 ProPheArgProCysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPheThr 376
DB 718 CTTTAAACCTCTGTGCAATCTGAAGAGATGTAAGTCACTTGAATTCAGATTACA 777
QY 377 ArgGlnThrProValAspSerProAspAspThrAlaLeuSerGluSerAlaSerGlnAla 396
DB 778 CGTGAGACACCTGTGAGACGCCAGATGACGCACTCAGTGAAACTGCCAATCAGGCTC 837
QY 397 PheLeu 398
DB 838 TTCTG 843
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Search completed: July 3, 2004, 13:52:59  
Job time : 711 secs



QY 206 CTGCGAGTTGAGGCGAGCTGGCTAGAGCTGTGGGACATATGAAAGGTGAGCTG 265  
 Db 152 CTGCGAGTTGAGGCGAGCTGGCTAGAGCTGTGGGACATATGAAAGGTGAGCTG 211  
 QY 266 ACTGAGACCAAGCTGTAAGCTTGGCCGAGAGCGCATGGGCCCCCATCTGTGAGCTG 325  
 Db 212 ACTGAGACCAAGCTGTAAGCTTGGCCGAGAGCGCATGGGCCCCCATCTGTGAGCTG 271  
 QY 326 CGTGTGCTGGGCAAGGGGGGCTATGGCAAGTGTCTCAGGTGGGAAAGGTGCAAGGCGC 385  
 Db 272 CGTGTGCTGGGCAAGGGGGGCTATGGCAAGTGTCTCAGGTGGGAAAGGTGCAAGGCGC 331  
 QY 386 AACTTGGGCAAAATATATGCTATGAAAGTCTTAAGGAGGCGCAAAATGTGGCAATGCG 445  
 Db 332 AACTTGGGCAAAATATATGCTATGAAAGTCTTAAGGAGGCGCAAAATGTGGCAATGCG 391  
 QY 446 AAGGACACAGGCAACACAGGGGCTGAGCGGGAATCTTAGAGTCAATGAAAGCGCCCTTT 505  
 Db 392 AAGGACACAGGCAACACAGGGGCTGAGCGGGAATCTTAGAGTCAATGAAAGCGCCCTTT 451  
 QY 506 ATTGTGGAATCTGCTATGCTTCAAGCTGTGGGCAAACTTACCTCACTCTTGAAGTGC 565  
 Db 452 ATTGTGGAATCTGCTATGCTTCAAGCTGTGGGCAAACTTACCTCACTCTTGAAGTGC 511  
 QY 566 CTGAGTGTGGCGAGCTTCTCAAGCATCTGGAGCGAGAGGCGATCTTCTGGAAGTAG 625  
 Db 512 CTGAGTGTGGCGAGCTTCTCAAGCATCTGGAGCGAGAGGCGATCTTCTGGAAGTAG 571  
 QY 626 GCTGTCTTACTGCTGCTGAGATCAAGCTGGCCCTGGGCAATCTCCAGGAGCATG 685  
 Db 572 GCTGTCTTACTGCTGCTGAGATCAAGCTGGCCCTGGGCAATCTCCAGGAGCATG 631  
 QY 686 ATCTACCGGAGCCTCAAGCCCGAGAAATCATATCTCAGAGCCAGGCGCAATCAAACTG 745  
 Db 632 ATCTACCGGAGCCTCAAGCCCGAGAAATCATATCTCAGAGCCAGGCGCAATCAAACTG 691  
 QY 746 ACCGACTTTGAGCTGCAAGAGTCTATCATGAGGCGCGCTCACTCAACCTTCTGC 805  
 Db 692 ACCGACTTTGAGCTGCAAGAGTCTATCATGAGGCGCGCTCACTCAACCTTCTGC 751  
 QY 806 GGCACCATTTGAGTACATGCGCCCTGAGATTTCTGTGGCGAGTGGCCACACCGGGCTGTG 865  
 Db 752 GGCACCATTTGAGTACATGCGCCCTGAGATTTCTGTGGCGAGTGGCCACACCGGGCTGTG 811  
 QY 866 GACTGTGAGGCTGGGGGGCCCTGATGTAAGATCAATGCTCACTGAGATGGCGCCCTTAC 925  
 Db 812 GACTGTGAGGCTGGGGGGCCCTGATGTAAGATCAATGCTCACTGAGATGGCGCCCTTAC 871  
 QY 926 GCAGAGAACCGGAAAGAAACCATGATTAAGATCATAGGGGCAAGCTGGCACTGCCGCC 985  
 Db 872 GCAGAGAACCGGAAAGAAACCATGATTAAGATCATAGGGGCAAGCTGGCACTGCCGCC 931  
 QY 986 TACCTACCCAGATGCCCGGAGCCTTGTCAAAATTTCTGAAACGGAATCCGAGCCG 1045  
 Db 932 TACCTACCCAGATGCCCGGAGCCTTGTCAAAATTTCTGAAACGGAATCCGAGCCG 991  
 QY 1046 CGGATTGGGGGTGGCCCAAGGGAGTGTGTGATGTGCAAGACATCCCTTTTTCGGGAC 1105  
 Db 992 CGGATTGGGGGTGGCCCAAGGGAGTGTGTGATGTGCAAGACATCCCTTTTTCGGGAC 1051  
 QY 1106 ATGAAATTTGGAACACCTTCTGCGCTGGCGGTGGAGACCCCTTTCAAGGCGCTGTGAG 1165  
 Db 1052 ATGAAATTTGGAACACCTTCTGCGCTGGCGGTGGAGACCCCTTTCAAGGCGCTGTGAG 1111  
 QY 1166 TCAGAGAGAGCTGAGCAGCTTGTATACCCGCTTCAACAGGACAGCGCGGTGACAGT 1225  
 Db 1112 TCAGAGAGAGCTGAGCAGCTTGTATACCCGCTTCAACAGGACAGCGCGGTGACAGT 1171  
 QY 1226 CCGGATGACACAGCCCTTGAAGGAGTGGCAACAGGCGCTTCTGTGGCTTCAACATGCG 1285  
 Db 1172 CCGGATGACACAGCCCTTGAAGGAGTGGCAACAGGCGCTTCTGTGGCTTCAACATGCG 1231  
 QY 1286 GCGCGCTGTGTCTGTGACAGCATCAAGAGGGCTTCTTCCATCCAGCCCAAGCTGCGCTCA 1345

Db 1232 GCGCGCTGTGTCTGTGACAGATCAAGAGGGCTTCTCTTCCAGCCCAAGCTGCGCTCA 1291  
 QY 1346 CCGAGGCGCTTCAACAGTATAGCCCCCGGGTCCCGGTCAAGCCCTCAAGTCTCCCTTTT 1405  
 Db 1292 CCGAGGCGCTTCAACAGTATAGCCCCCGGGTCCCGGTCAAGTCTCCCTTTT 1351  
 QY 1406 GAGGGGTTTCCGCGCCAGCCCAAGCTGCGGAGCCACGAGCTACCTTCACTCACTC 1465  
 Db 1352 GAGGGGTTTCCGCGCCAGCCCAAGCTGCGGAGCCACGAGCTACCTTCACTCACTC 1411  
 QY 1466 CTGCAACCGCGCGCCCTTCAAGACCCGCTTCTCCCATCTCCGTCCCTCCAGAGAC 1525  
 Db 1412 CTGCAACCGCGCGCCCTTCAAGACCCGCTTCTCCCATCTCCGTCCCTCCAGAGAC 1471  
 QY 1526 AAGAGTCTCAAGAGGGGCGGTGGGCTGCAAGGCGCTAGGAAGCGGGTGGGGTGAAGG 1585  
 Db 1472 AAGAGTCTCAAGAGGGGCGGTGGGCTGCAAGGCGCTAGGAAGCGGGTGGGGTGAAGG 1531  
 QY 1586 TAGCCCTTGAAGCCCTGTCTGCGGCTGTGAGAGCAAGACCTTGGGCCATGTTCCAGA 1645  
 Db 1532 TAGCCCTTGAAGCCCTGTCTGCGGCTGTGAGAGCAAGACCTTGGGCCATGTTCCAGA 1591  
 QY 1646 GACCTGGGGGTGTGTCTGGGGGTGGGGGTGTGAGTGCATGAAAGTGTGTCTGCTGG 1705  
 Db 1592 GACCTGGGGGTGTGTCTGGGGGTGGGGGTGTGAGTGCATGAAAGTGTGTCTGCTGG 1651  
 QY 1706 GCAAGCTGACCCCTGTAATCATGAGGCAAGAGGGCGGCCGCAACCCCGGCTCACTG 1765  
 Db 1652 GCAAGCTGACCCCTGTAATCATGAGGCAAGAGGGCGGCCGCAACCCCGGCTCACTG 1711  
 QY 1766 CTCCCGTGAAGATTAAGGGCTGAATCATG 1796  
 Db 1712 CTCCCGTGAAGATTAAGGGCTGAATCATG 1742

RESULT 2  
 US-09-925-298-245  
 ; Sequence 245, Application US/09925298  
 ; Publication No. US20020039764A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA103  
 ; CURRENT APPLICATION NUMBER: US/09/925,298  
 ; PRIOR FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05881  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124,270  
 ; NUMBER OF SEQ ID NOS: 846  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 245  
 ; LENGTH: 1197  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (218)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1193)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; US-09-925-298-245

Query Match 63.8%; Score 1158.6; DB 13; Length 1197;  
 Best Local Similarity 99.3%; Pred. No. 5,6e-302;  
 Matches 1180; Conservative 3; Mismatches 3; Indels 2; Gaps 2;

Db 624 GCGCTGCTTACTGCTGAGATCAAGCTGGCGCCCGGCGCATCTCCAGGGCA 683  
 11 GCGCTGCTTACTGCTGAGATCAAGCTGGCGCCCGGCGCATCTCCAGGGCA 70

QY 684 TCATCTACCGGAGCTTCAAGCCCGAGAAATCATATGCTTCAAGCCAGGAGCAATCAAC 743  
 Db 71 TCATCTACCGGAGCTTCAAGCCCGAGAAATCATATGCTTCAAGCCAGGAGCAATCAAC 130  
 QY 744 TGACGAGCTTGGAGCTTGCAGAGAGTATCATAGAGGAGCGGTCACTCAACCTTCT 803  
 Db 131 TGACGAGCTTGGAGCTTGCAGAGAGTATCATAGAGGAGCGGTCACTCAACCTTCT 190  
 QY 804 GCGGACCATTTAGATCAATGCCCCCTG-AGATTCTGTGTGCGAGTGGCCACACCGGGCT 862  
 Db 191 GCGGACCATTTAGATCAATGCCCCCTGAGATTCTGTGTGCGAGTGGCCACACCGGGCT 250  
 QY 863 GTGAGCTGTGAGAGCTGGGGGCGCTATGTAAGACATGCTCACTGATGATGCGCGCCCTT 922  
 Db 251 GTGAGCTGTGAGAGCTGGGGGCGCTATGTAAGACATGCTCACTGATGATGCGCGCCCTT 310  
 QY 923 ACCGAGAGAACCGGAGAGAAACCATGATTAAGATCATCAGGGGCAAGCTTGACCTGCC 982  
 Db 311 ACCGAGAGAACCGGAGAGAAACCATGATTAAGATCATCAGGGGCAAGCTTGACCTGCC 370  
 QY 983 CCCTAAGCTCAACCCAGATGCCCCGGGACCTTGTGAAAAAGTTTCTGAAAACGGAATCCGAGC 1042  
 Db 371 CCCTAAGCTCAACCCAGATGCCCCGGGACCTTGTGAAAAAGTTTCTGAAAACGGAATCCGAGC 430  
 QY 1043 CAGCGAATGGGGGTGGCCCAAGGGAGATGCTGATGATGAGAGACATCCCTTTTTCGCG 1102  
 Db 431 CAGCGAATGGGGGTGGCCCAAGGGAGATGCTGATGATGAGAGACATCCCTTTTTCGCG 490  
 QY 1103 CACATGAATTGGAGACGACCTTCTGGGCTGGGCTGTGGAACCCCTTTCAAGGCTGTCTG 1162  
 Db 491 CACATGAATTGGAGACGACCTTCTGGGCTGGGCTGTGGAACCCCTTTCAAGGCTGTCTG 550  
 QY 1163 CAGTCAAGAGAGAGCTGAGACAGTTTATACCCGCTTTCACACGCGAGAGCGCGTGGAGC 1222  
 Db 551 CAGTCAAGAGAGAGCTGAGACAGTTTATACCCGCTTTCACACGCGAGAGCGCGTGGAGC 610  
 QY 1223 AGTCTGTATGACACAGCCCTTCAAGAGAGTGGCAACAGGCTTCTGAGGCTTTCACATAC 1282  
 Db 611 AGTCTGTATGACACAGCCCTTCAAGAGAGTGGCAACAGGCTTCTGAGGCTTTCACATAC 670  
 QY 1283 GTGGGCGCGCTGTGCTCTGAGACAGATGTAAGAGGGGCTTCTCTCAAGCCCAAGCTGGC 1342  
 Db 671 GTGGGCGCGCTGTGCTCTGAGACAGATGTAAGAGGGGCTTCTCTCTCAAGCCCAAGCTGGC 730  
 QY 1343 TCACCCAGGCGCTTCAACATGAGGCCCCGGGCTCCCGTCAAGCCCTTCAAGTTCCTCT 1402  
 Db 731 TCACCCAGGCGCTTCAACATGAGGCCCCGGGCTCCCGTCAAGGCTTCTCTCTCT 790  
 QY 1403 TTTGAGAGGGTTTGGGCGCCAGAGCCCAAGCTTCCCGAGGCCCAAGGCTTCACTTCA 1462  
 Db 791 TTTGAGAGGGTTTGGGCGCCAGAGCCCAAGCTTCCCGAGGCCCAAGGCTTCACTTCA 850  
 QY 1463 CTCCTGCAACGCGCGCGCTTGCAGACACGCGCTTCTCCCATCCGTCCTCCCTCAAGG 1522  
 Db 851 CTCCTGCAACGCGCGCGCTTGCAGACACGCGCTTCTCCCATCCGTCCTCCCTCAAGG 910  
 QY 1523 ACCAAGAGTCCAAAGAGGGGCGGTGGCGCTTCAAGGCGCTTCAAGAGGCTGGGTGTA 1582  
 Db 911 ACCAAGAGTCCAAAGAGGGGCGGTGGCGCTTCAAGGCGCTTCAAGAGGCTGGGTGTA 970  
 QY 1583 GGGTAGGCTTGAAGCTTGTCTGCGGGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1642  
 Db 971 GGGTAGGCTTGAAGCTTGTCTGCGGGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1030  
 QY 1643 AGAGAGCTGGGGGTGTGTCTGGGGGTGGGGGTGTGAGTGTGATGAAAGTGTGTCTGCT 1702  
 Db 1031 AGAGAGCTGGGGGTGTGTCTGGGGGTGGGGGTGTGAGTGTGATGAAAGTGTGTCTGCT 1090  
 QY 1703 GGGGAGCTGTGCGCTTCAAG 1762  
 Db 1091 GGGGAGCTGTGCGCTTCAAG 1149  
 QY 1763 CTGCTCCGCGAGAGATTAAGGGCTGAATCATGAAAAAATGAAAAA 1810

Db 1150 CTGCTCCGCGAAGATTAAGGGCTGAATCATGAAAAAATGAAAAA 1197  
 RESULT 3  
 US-10-102-806-245  
 ; Sequence 245, Application US/10102806  
 ; Publication No. US2003005421A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: P4103P1  
 ; CURRENT APPLICATION NUMBER: US/10/102, 806  
 ; PRIOR FILING DATE: 2002-03-22  
 ; PRIOR APPLICATION NUMBER: 09/925, 298  
 ; PRIOR FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05881  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124,270  
 ; NUMBER OF SEQ ID NOS: 846  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 245  
 ; LENGTH: 1197  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (218)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1193)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 US-10-102-806-245  
 Query Match 63.8%; Score 1158.6; DB 15; Length 1197;  
 Best Local Similarity 99.3%; Pred. No. 6,6e-302;  
 Matches 1180; Conservative 3; Mismatches 3; Indels 2; Gaps 2;  
 QY 624 CGGCGCTTCTTCAACCTGCTGAGATCAGCTGGCCCTGGGACATCCACAGGGA 683  
 Db 11 CGGCGCTTCTTCAACCTGCTGAGATCAGCTGGCCCTGGGACATCCACAGGGA 70  
 QY 684 TCATCTACCGGAGCTTCAAGCCCGAGAAATCATATGCTTCAAGCCAGGAGCAATCAAC 743  
 Db 71 TCATCTACCGGAGCTTCAAGCCCGAGAAATCATATGCTTCAAGCCAGGAGCAATCAAC 130  
 QY 744 TGACGAGCTTGGAGCTTGCAGAGAGTATCATAGAGGAGCGGTCACTCAACCTTCT 803  
 Db 131 TGACGAGCTTGGAGCTTGCAGAGAGTATCATAGAGGAGCGGTCACTCAACCTTCT 190  
 QY 804 GCGGACCATTTAGATCAATGCCCCCTG-AGATTCTGTGTGCGAGTGGCCACACCGGGCT 862  
 Db 191 GCGGACCATTTAGATCAATGCCCCCTGAGATTCTGTGTGCGAGTGGCCACACCGGGCT 250  
 QY 863 GTGAGCTGTGAGAGCTGGGGGCGCTATGTAAGACATGCTCACTGATGATGCGCGCCCTT 922  
 Db 251 GTGAGCTGTGAGAGCTGGGGGCGCTATGTAAGACATGCTCACTGATGATGCGCGCCCTT 310  
 QY 923 ACCGAGAGAACCGGAGAGAAACCATGATTAAGATCATCAGGGGCAAGCTTGACCTGCC 982  
 Db 311 ACCGAGAGAACCGGAGAGAAACCATGATTAAGATCATCAGGGGCAAGCTTGACCTGCC 370  
 QY 983 CCCTAAGCTCAACCCAGATGCCCCGGGACCTTGTGAAAAAGTTTCTGAAAACGGAATCCGAGC 1042  
 Db 371 CCCTAAGCTCAACCCAGATGCCCCGGGACCTTGTGAAAAAGTTTCTGAAAACGGAATCCGAGC 430  
 QY 1043 CAGCGAATGGGGGTGGCCCAAGGGAGATGCTGATGATGAGAGACATCCCTTTTTCGCG 1102  
 Db 431 CAGCGAATGGGGGTGGCCCAAGGGAGATGCTGATGATGAGAGACATCCCTTTTTCGCG 490  
 QY 1103 CACATGAATTGGAGACGACCTTCTGGGCTGGGCTGTGGAACCCCTTTCAAGGCTGTCTG 1162











; NUMBER OF SEQ ID NOS: 1140  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 230  
 ; LENGTH: 2287  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 ; FEATURE:  
 ; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM\_031985  
 US-10-191-803-230

Query Match 34.8%; Score 628.2; DB 16; Length 2287;  
 Best Local Similarity 71.1%; Pred. No. 6,3e-159;  
 Matches 83; Conservative 0; Mismatches 338; Indels 0; Gaps 0;

QY 240 TGGGACCTATGAGAGAGTGGAGCTGAGACCAAGCTGAAAGTGGCCAGAGCGCA 299  
 DB 218 TGGAACTGTGTGAGAAATTTGAAATCTCAAGAACTAGTGTGAACAGAGGCCAGAAAAA 277  
 QY 300 TCGGGCCCACTGTTTGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 359  
 DB 278 TCGAACCAAGATTTTGTGACTTCTGAGTACTTGTGTGTGTGTGTGTGTGTGTGTGTGT 337  
 QY 360 TCGAGGTGCGAAAGGTGCGAAGCAACCACTTGGGCAAAATATATGTCATGAAAGTCTAA 419  
 DB 338 TCGAAGTACGAAAGTACAGAGCAAAATCTGGAAAGATATTTGCCATGAAAGTCTTA 397  
 QY 420 GGAAGGTCAAAATTTGTGCGAATGCCAGAGCAAGCAAGCAAGCGGCTGAGCGGAACA 479  
 DB 398 AAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 457  
 QY 480 TTCTAGAGTGTGAGAGCAACCCCTTATTTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 539  
 DB 458 TTCTGAGAGAGTAAAGCAATCCCTTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 517  
 QY 540 GCAAACTTATCTCTATCTCTTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 599  
 DB 518 GAAAACTTATCTCTATCTCTTGAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 577  
 QY 600 GAGAGGCACTCTCTCTGAAAGATAGAGGCTGTCTTACCTGGGTGTGTGTGTGTGTGTGTGTGT 659  
 DB 578 GAGAGGCACTCTCTCTGAAAGATAGAGGCTGTCTTACCTGGGTGTGTGTGTGTGTGTGTGTGT 637  
 QY 660 TGGGCACTCTCTCTCTGAAAGATAGAGGCTGTCTTACCTGGGTGTGTGTGTGTGTGTGTGTGT 719  
 DB 638 TGGGCACTCTCTCTCTGAAAGATAGAGGCTGTCTTACCTGGGTGTGTGTGTGTGTGTGTGTGT 697  
 QY 720 TCAAGGCACTCTCTCTCTGAAAGATAGAGGCTGTCTTACCTGGGTGTGTGTGTGTGTGTGTGTGT 779  
 DB 698 TTAATACCAAGTCTCTCTCTGAAAGATAGAGGCTGTCTTACCTGGGTGTGTGTGTGTGTGTGTGT 757  
 QY 780 AGGAGCGCGTCACTCAACCTTGTGCGGCAACATTTAGTAATGATGATGATGATGATGATGATGAT 839  
 DB 758 ATGGAACAGTCAAGCACTCTTGTGGAACAATTAATTAATTAATTAATTAATTAATTAATTAAT 817  
 QY 840 TGGGCACTCTCTCTCTCTGAAAGATAGAGGCTGTCTTACCTGGGTGTGTGTGTGTGTGTGTGTGT 899  
 DB 818 TGGGCACTCTCTCTCTCTGAAAGATAGAGGCTGTCTTACCTGGGTGTGTGTGTGTGTGTGTGTGT 877  
 QY 900 TGGTCACTGATGAGCGGCTTATACCGCAGAGAACCGAAGAAACCATGATTAAGATCA 959  
 DB 878 TGGTCACTGATGAGCGGCTTATACCGCAGAGAACCGAAGAAACCATGATTAAGATCA 937  
 QY 960 TCGAGGCGCAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1019  
 DB 938 TCGAAGTAACTTAATTTGCT 997  
 QY 1020 AGTTTCTGAAACCGAAATCCAGCAGCGAATGGGGGTGGCCAGGGGAATGCTGTGATG 1079  
 DB 998 AGCTGTGAAAGAAATGCTGTCT 1057  
 QY 1080 TCGAGAGATATCCCTTTTCCGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1139  
 DB 1058 TCGAAGCGATTCATTTTGAACATTAATCTGGGAAGAGCTTTTGTGTGTGTGTGTGTGTGTGTGT 1117

QY 1140 ACCCCCTTTGAGGCGCTTCTGAGTCAAGAGAGAGTGAAGCCAGTTTGAATACCGCT 1199  
 DB 1118 AGCGCCCTTTAAGCTGT 1177  
 QY 1200 TCAACAGGAGACCGCGGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1259  
 DB 1178 TTAATCTGTCAGACACTGT 1237  
 QY 1260 AGGCTTCTGAGGCTTCAATATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1319  
 DB 1238 AGCTTCTTGT 1297  
 QY 1320 TCTCTTCCAGCCCAAGT 1379  
 DB 1298 TTTCTTTTGAACCAAAATCCGATGCTGTGAAGATTAATGTGTGTGTGTGTGTGTGTGTGTGT 1357  
 QY 1380 TCAAGCCCTCAAGTGTCTCCCTTTGA 1407  
 DB 1358 TCAAGCCCAATCTCTCTCTGAGGA 1385

RESULT 10  
 US-09-954-456-1137  
 ; Sequence 1137, Application us/09954456  
 ; Patent No. US20020115057A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, Paul  
 ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C  
 ; FILE REFERENCE: 689290-76  
 ; CURRENT APPLICATION NUMBER: US/09/954,456  
 ; PRIOR FILING DATE: 2001-09-18  
 ; PRIOR APPLICATION NUMBER: US/60/233,617  
 ; PRIOR FILING DATE: 2000-09-18  
 ; PRIOR APPLICATION NUMBER: US/60/234,052  
 ; PRIOR FILING DATE: 2000-09-20  
 ; PRIOR APPLICATION NUMBER: US/60/234,923  
 ; PRIOR FILING DATE: 2000-09-25  
 ; PRIOR APPLICATION NUMBER: US/60/235,134  
 ; PRIOR FILING DATE: 2000-09-25  
 ; PRIOR APPLICATION NUMBER: US/60/235,637  
 ; PRIOR FILING DATE: 2000-09-26  
 ; PRIOR APPLICATION NUMBER: US/60/235,638  
 ; PRIOR FILING DATE: 2000-09-26  
 ; PRIOR APPLICATION NUMBER: US/60/235,711  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: US/60/235,720  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: US/60/235,840  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: US/60/235,863  
 ; PRIOR FILING DATE: 2000-09-27  
 ; NUMBER OF SEQ ID NOS: 2276  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1137  
 ; LENGTH: 2346  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-954-456-1137

Query Match 34.1%; Score 619.8; DB 9; Length 2346;  
 Best Local Similarity 70.5%; Pred. No. 1.2e-156;  
 Matches 824; Conservative 0; Mismatches 344; Indels 0; Gaps 0;

QY 240 TGGACACTATGAGAGTGTGAGCTGATGAGACCAAGCTGAAAGCTTGGCCAGAGCGCA 299  
 DB 224 TGAACATTTGAGAGAAATTTGAAATCTCAAGAACTAGTGTGAACAGAGGCGCAAGAAAAA 283  
 QY 300 TCGGCGCCCACTGT 359  
 DB 284 TGAAGCAAGATTTTGAAGT 343

QY 360 TCCAGGTCGAAAGGTGCAAGGCAACCACTTGGGCAAAATATATGCCATGAAAGTCTTAA 419  
 Db 344 TTCAAGTACGAAAGATACAGAGCAAAATACCTGGGAAATATTTGCCATGAAAGTGTCTTA 403  
 QY 420 GGAAGGCGCAAAATGTGCGCAATGCGAGCAACAGGCAACACCGGCTGTAGGGGAA 479  
 Db 404 AAAAGGCAATGATATGAAATGCTAAAGATACAGCTCATACAAAAGCAAGCAAGATA 463  
 QY 480 TTCTAGAGTCAGTGAAGCAACCCCTTATTTGGAACCTGAGCTATGCTTCCAGATGAGT 539  
 Db 464 TTCTGAGAGAGTAAAGCATCCCTTCATCGTGAATTTATTTATGCTTTCAGACTGAGT 523  
 QY 540 GCAAACTTACTGATCTTGAAGTCTTGAAGTCTGAGTGTGAGGAGCTTTCAGCATTTGAGC 599  
 Db 524 GAAAACTTACTGATCTTGAAGTCTTGAAGTCTGAGTGTGAGGAGCTTTCAGCATTTGAGC 583  
 QY 600 GAGAGGAGCATCTTCTGGAAGATAGGAGCTGCTTCTACCTGAGTGAATCAAGCTGAGCC 659  
 Db 584 GAGAGGAGATTTATGGAAGACATGCTGCTGCTTTTCTTGGCAAGATCTCCAGTGGCTT 643  
 QY 660 TGGGCAATCTCCACTCCAGGCAATCATCTACCGGCACTTCAAGCCCGAGAAATCATGTC 719  
 Db 644 TGGGCAATTTACATCAAAAGGAGATCATCTACAGAGACCTGAAGCCGAGAAATTCATGTC 703  
 QY 720 TCAGCAGCAGGCGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 779  
 Db 704 TTAATCAACAGATCTGATGAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 763  
 QY 780 AGGCGCGCTGCTACTCAGACCTTTCGCGGCAACATTTAGTACATAGGCTTCAAGATTCG 839  
 Db 764 ATGGAAGTCAACACACATTTTGTGAAACATTAAGATACATAGGCTTCAAGATTCG 823  
 QY 840 TGGGCAATGCGCAACACCGGCTGTGAGCTGTGAGAACCTTGGGCGCTTATGATGACA 899  
 Db 824 TGAAGATGCGCAACATGCTGTGAGATGCTGTGAGATTTGGAGCAATTAATGATGACA 883  
 QY 900 TGCTCACTGATGCGCCCTTTTACCGAGAAACCGGAAGAAACCATGATTAAGTCA 959  
 Db 884 TGCTGATGAGAGACCCCTTCACTGCGGAGAAATGAAGAAACCATGATTAAGTCA 943  
 QY 960 TCAGGCGCAAGCTGAGCACTGCGCTTCACTCAGCCGAAATGCCGCGGACCTTGTGAAA 1019  
 Db 944 TCAATGTAACATCAATTTGCTTCTTCACTCAGCAAGAGCCAGAGATCTGCTTAAA 1003  
 QY 1020 AGTTTCTGAACGGAATCCAGAGCAAGGATTTGGGCGGTGGCCAGGGGATGCTGTGATG 1079  
 Db 1004 AGCTGCTGAAGAAATGCTGCTTCTGCTGGAAGCTTGTCTTGGGAGAGAG 1063  
 QY 1080 TGAGAGACATCCCTTTTTCGCGCAATGAATTTGGAGCACTTGTGCGCTGTGCGTGTG 1139  
 Db 1064 TTCAAGCTCATTCATCTTTAGACACATTAATGAGGAAACCTTGTGCGCTGAAAGGTG 1123  
 QY 1140 ACCGCCCTTCAAGGCGCTGTGAGCAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1199  
 Db 1124 AGCCGCCCTTAAACCTGTGTGAAATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1183  
 QY 1200 TCAACGCGAGAGCGCGGTGAGAGATCTGATGACACAGCCCTCAGCGAGAGTGGCAAC 1259  
 Db 1184 TTAACGTCAGACACCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1243  
 QY 1260 AGGCTTCTGCGCTTCACTACATGATGAGCGCGCTGTGCTGTGAGAGAGAGAGAGAG 1319  
 Db 1244 AGGCTTCTGCGCTTCACTACATGATGAGCGCGCTGTGCTGTGAGAGAGAGAGAGAG 1303  
 QY 1320 TCTCTCTCAAGCCCAAGCTGCGCTCAACAGAGCGCTCAACAGTAAAGCCCGAGTCCCG 1379  
 Db 1304 TTCTCTTTGAACCAAAATCCGATCACTGTGAAGATTTATTTGCAAGCCCAAGAGAGAG 1363  
 QY 1380 TCAGCCCGCTCAAGTCTTCCCTTTTGA 1407  
 Db 1364 TCAGCCCAAGCAATTTTCTCTGAGGGA 1391

RESULT 11  
 US-09-920-677-3  
 ; Sequence 3, Application US/0920677  
 ; Publication No. US20030083284A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bret P. Monia  
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF P70 S6 KINASE EXPRESSION  
 ; FILE REFERENCE: RTS-0245  
 ; CURRENT APPLICATION NUMBER: US/09/920,677  
 ; NUMBER OF SEQ ID NOS: 45  
 ; SEQ ID NO 3  
 ; LENGTH: 2346  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (28)...(1605)  
 ; US-09-920-677-3  
 Query Match 34.1%; Score 619.8; DB 10; Length 2346;  
 Best Local Similarity 70.5%; Pred. No. 1,2e-156;  
 Matches 824; Conservative 0; Mismatches 344; Indels 0; Gaps 0;  
 QY 240 TGGGCACTATGAAAGGTGAGAGCTGATGAGACCAAGCTGAACGTTGGCCCAAGAGCA 239  
 Db 224 TGGGCACTATGAGAAATTTGAAATCTCAGAACTGATGAGACAGAGGCGCAAGAAAA 283  
 QY 300 TGGGCGCCCACTGCTTGTGAGCTGCTGCTGTGCTGAGGAGGAGGCTATGAGAGGTG 359  
 Db 284 TGGGCGCCCACTGCTTGTGAGCTGCTGCTGTGCTGAGGAGGAGGCTATGAGAGGTG 343  
 QY 360 TCGAGTGGCAAGGTGCAAGCACTTGGGCAAAATATATGCGATGAAATGCTTAA 419  
 Db 344 TTCAAGTACGAAAGATACAGAGCAAAATACCTGGGAAATATTTGCCATGAAAGTGTCTTA 403  
 QY 420 GGAAGGCGCAAAATGTGCGCAATGCGAGCAACAGGCAACACCGGCTGTAGGGGAA 479  
 Db 404 AAAAGGCAATGATATGAAATGCTAAAGATACAGCTCATACAAAAGCAAGCAAGATA 463  
 QY 480 TTCTAGAGTCAGTGAAGCAACCCCTTATTTGGAACCTGAGCTATGCTTCCAGATGAGT 539  
 Db 464 TTCTGAGAGAGTAAAGCATCCCTTCATCGTGAATTTATTTATGCTTTCAGACTGAGT 523  
 QY 540 GCAAACTTACTGATCTTGAAGTCTTGAAGTCTGAGTGTGAGGAGCTTTCAGCATTTGAGC 599  
 Db 524 GAAAACTTACTGATCTTGAAGTCTTGAAGTCTGAGTGTGAGGAGCTTTCAGCATTTGAGC 583  
 QY 600 GAGAGGAGCATCTTCTGGAAGATAGGAGCTGCTTCTACCTGAGTGAATCAAGCTGAGCC 659  
 Db 584 GAGAGGAGATTTATGGAAGACATGCTGCTGCTTTTCTTGGCAAGATCTCCAGTGGCTT 643  
 QY 660 TGGGCAATCTCCACTCCAGGCAATCATCTACCGGCACTTCAAGCCCGAGAAATCATGTC 719  
 Db 644 TGGGCAATTTACATCAAAAGGAGATCATCTACAGAGACCTGAAGCCGAGAAATTCATGTC 703  
 QY 720 TCAGCAGCAGGCGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 779  
 Db 704 TTAATCAACAGATCTGATGAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 763  
 QY 780 AGGCGCGCTGCTACTCAGACCTTTCGCGGCAACATTTAGTACATAGGCTTCAAGATTCG 839  
 Db 764 ATGGAAGTCAACACACATTTTGTGAAACATTAAGATACATAGGCTTCAAGATTCG 823  
 QY 840 TGGGCAATGCGCAACACCGGCTGTGAGCTGTGAGAACCTTGGGCGCTTATGATGACA 899  
 Db 824 TGAAGATGCGCAACATGCTGTGAGATGCTGTGAGATTTGGAGCAATTAATGATGACA 883  
 QY 900 TGCTCACTGATGCGCCCTTTTACCGAGAAACCGGAAGAAACCATGATTAAGTCA 959  
 Db 884 TGCTGATGAGAGACCCCTTCACTGCGGAGAAATGAAGAAACCATGATTAAGTCA 943







Db 632 GTGGAAGCTCTTACACAGTGTCTTAACAGAACCATCTCATTTGGGCTTTCTTC 691  
 QY -----TGTCTTACCTGGCTAGATCAAGCTGGGCTGGGCTATCTCCAGGG 681  
 Db 692 CTGGAATGCTTTTACTTGGGAGAAATCTCCATGCTTTGGGGATTTTACCAAAAGG 751  
 QY 682 CATCATCTACCGGAGCTTCAAGCCGAGAAACATCATGCTCAGAGCCAGGCGCATCAA 741  
 Db 752 GATCATCTACAGAGACTTGAAGCCGAGAAATCATGCTTTAATCAACAGGTCATGTGA 811  
 QY 742 ACTGACCGACTTTGAGCTCTGCAAGAGCTTATCCATGAGGCGGCTGATCAACCTT 801  
 Db 812 ACTAAGACCTTTGAGCTATGCAAGAACTTATTCATGAGAACGTACACACATTT 871  
 QY 802 CTGCGGACCATTTAGATACATGAGCCCTGAGATTCGTGTGCGAGTGGCACAACCGAGC 861  
 Db 872 TTGTGGAACATGATATACATGAGCCCTGAAATCTTATGAGAAAGTGGCACAATGTGC 931  
 QY 862 TGTGACCTGTGAGAGCTGGGGGCTCTGATGTACAGCATGCTCATCTGATTCGCGCTT 921  
 Db 932 TGTGATTTGTGAGTTTGGAGCATTAATGATGACATGTGACTGAGGACCCCATTT 991  
 QY 922 TACCGAGAAACCGAGAAACCATGATTAAGATCATAGGGGCAAGCTGCACTGCC 981  
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 ; Patent No. US20010042254A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Stewart, Mary  
 ; APPLICANT: Kozma, Sarah  
 ; APPLICANT: Thomas, George  
 ; TITLE OF INVENTION: Drosophila Melanogaster P70 S6 Kinase  
 ; FILE REFERENCE: 4-20971/A  
 ; CURRENT APPLICATION NUMBER: US/09/817,310  
 ; CURRENT FILING DATE: 2001-03-26  
 ; PRIOR APPLICATION NUMBER: 09/230,247  
 ; PRIOR FILING DATE: 1999-04-16

; NUMBER OF SEQ ID NOS: 5  
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 ; ORGANISM: Drosophila melanogaster  
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